

FIGURE 1

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTGCTGTTTCTT  
CTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCG  
GCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACCTGGTGTACGGATGAAACCGTATGCCC  
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAG  
AGAAAGTGTGAGGTCAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCAT  
CAACCACGACCCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACC  
CCTTCACCATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCTGTGCGCCGCCGC  
CTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG  
CACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCCCCGAGACCATCCTCCTTGACCTTT  
GTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAGCAAG

1000157.031502

2/71

FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYERNIEEMVA  
QLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTMQEDRSMVSV  
VFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

10000157.031503  
20570" 2570000T

FIGURE 3

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCC  
TGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGGCACCCCCACAGTCAC  
GGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGG  
TGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGC  
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC  
CAGCGCTCCATCTCACCCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT  
CGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGC  
GGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT  
GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGCACCTGCGTGCTGCCCCGTTTCAGT  
GTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTG  
TATTTATTGTTATTTATATGCCTCCCCCAACTACCCCTGGGGTCTGGGCATTCCCCGTGTCTGGAGGAC  
AGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGC  
CCTTAAAGCTGCAGAAAAGGTGTACACGGCTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCT  
TACCCTATCACTGGCCTCAGGCCCCGAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTA  
AACAATTATTTAAGTGACGTGTATTATTAACTGATGAACACATCCCCAAAA

205157.031506

FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLE  
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAF AECLCRGCIDARTGRE  
TAALNSVRLQLSLLVLRRRPCSRDGSGGLTPGAF AFHTEFIHVPVGCTCVLPRSV

Signal peptide:	Amino acids 1-18
Tyrosine kinase phosphorylation site:	Amino acids 112-121
N-myristoylation sites:	Amino acids 32-38;55-61;133-139
Leucine zipper pattern:	Amino acids 3-25
Homologous region to IL-17:	Amino acids 99-195

1000152.0350  
"ESTED" 25T000T

FIGURE 5

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCAGTCA  
GTGCCCCGACTTGTGACTGAGTGTGCAGTGCCCGCATGTACCAGGTCAGTGCAGAGGGCTGCCTGAGGGCT  
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGCTGCCAGGTTTGGGGCTGG  
GGGCAAGTGAGTGAAGAACTGGGATCCAGGGGGAGGGTGCAGATGAGGGAGCGACCCAGATTAGGTGA  
GGACAGTTCTCTCATTAGCCTTTTTCCTACAGGTGGTTGCATTCTTGGCAATGGTCATGGGAACCCACACCT  
ACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT  
GTGCCTGTGCCTCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGA  
CCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGA  
CCTGTACCACGCCCCTTGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGG  
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACC  
CACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGTGT  
GATGGGCTAGCCGACCTGCTGGAGGCTGGTCCCTTTTTGGGAAACCTGGAGCCAGGTGTACAACCACTTG  
CCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCCTGTGAAGTGTCTGTCTGGAGCAGCAGGATCCCGGGAC  
AGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGC  
CGGAAGCTGGTGTCTGTCATTTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCCATTCTGGAGGCCACCA  
CTCCTGTCTCTTCTCTTTTTCCCATCCCCCTGCTACCCCTGGCCCAGCACAGGCACTTTCTAGATATTTCCCC  
CTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATTGTGTTGTTTACTCATCACTCAGTGAGCATCTACTTTGG  
GTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA  
GAGATTTATCCAAATAAATATCTTTATTTAAAAATGAAAAA

205750" 1570000

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPARPNRHP  
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR  
RPCHGEKGTGKGYCLERRLYRVSLACVCVRPRVMG

Signal peptide:

Amino acids 1-32

N-glycosylation site:

Amino acids 136-140

Tyrosine kinase phosphorylation site:

Amino acids 127-135

N-myristoylation sites:

Amino acids 44-50;150-156

10000157 "031502  
205TEN" 25T000T

FIGURE 7

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCGCGGGCGCCCCAGGGCGGGCAGGCG  
CCCCGCGCGGCCGCGGGGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGG  
CCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGC  
CCGGCAGGGGGCAGGCCCCGGCGACCGCCGCTTCCGGCCGCCCCACCAACCTGCGCAGCGTGTGCCCCGGGC  
CTACAGAATCTCCTACGACCCGGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCT  
GCCTGACCGGGCTGTTTCGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCGTGTCTACATGCCCACCGTCGTC  
CTGCGCCGCACCCCCGCTGCGCCGGCGGCCGTTCGCTCTACACCGAGGCCTACGTCACCATCCCCGTGGG  
CTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCCA  
AGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCGTGAGGCCGGTCCTGCCCCGGGAGGTCTCCCCGG  
CCCGCATCCCAGGCGCCCAAGCTGGAGCCGCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGCACC  
GAGCAAACCAAGTGCCGGAGCACACGCGCCGCTTTTCATGGAGACTCGTAAGCAGCTTCATCTGACACGG  
GCATCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGG  
GCATCCTGTGTGCGCCCCGCATGGAGGGTTTGGAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATC  
GGCTGCTGCGGGTGAGGGCGTGACTACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTTTT  
AAAGCAATCTAAAAATAATAATAAGTATAGCGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGA  
GGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTT  
ACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTCTGG  
CCTGGGTCTCTGAATTCAGCCTGTACCGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC  
TTCCTTCCACTGAAGGTCTTCACGGGCCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCA  
GGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGC  
ACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGA  
ACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCA  
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCTGTTTCTGCA  
TTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGTCTCTGAACACAATTATTTGT  
AAAAGTTAGTAGTTCTTTTTTAAATCATTAAGAGGCTTGCTGAAGGAT

10000157 "031502"

FIGURE 8

MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASC  
PAGGRPGDRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGCEEDVRFRSAPVYMPTVV  
LR RTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGAKLLLGPNDA PAGP

Signal peptide:

Amino acids 1-15

N-glycosylation sites:

Amino acids 68-72;181-185

Tyrosine kinase phosphorylation site:

Amino acids 97-106

N-myristoylation sites:

Amino acids 17-23;49-55;74-80;  
118-124

Amidation site:

Amino acids 21-25

205700157-031502

9/71

FIGURE 9

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCAT  
GGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA  
AAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC  
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGAAGTTGG  
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACCCTGGTCGTC  
CGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCTGGTGAAGTGTGGCTGCACCTG  
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

10000157-031502

10/71

FIGURE 10

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINENQRVSMS  
RNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSSVSFQ  
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

Amino acids 1-30

N-glycosylation site:

Amino acids 83-86

N-myristoylation sites:

Amino acids 106-111;136-141

10000157.031502  
POSTED 1/5/00

**FIGURE 11**

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGT  
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGAGAGCTTGA  
GGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCAACAGGGGACTATTCAATTTTGATGAATGTAAGC  
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAA  
CTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGGCCCTTCCAGACTCAGACCAGACCCTCTGGTG  
GTAAATGGACATTTTCCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAAT  
ATTCCCTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA  
CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTA  
AGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATC  
CAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGT  
GGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCA  
GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAAC  
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT  
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGC  
CCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAA  
TTTCTTCAAACCATTCAGAAAGTGAGGTCACTCCTTGAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGG  
TCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCA  
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCC  
CTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCACTCTGCACAAATACGTGGTGGTCTACTT  
TAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATG  
CCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGC  
CACGATGGCTGCTGCTCCTTGTAG

205129 157 031502

**FIGURE 12**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRDLRVEPVTTSVATGDYSILMNVS WV  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLC PQTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGT CGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHV KQQVSAGKRSQACHD  
GCCSL

Signal sequence:	Amino acids 1-14
Transmembrane domain:	Amino acids 290-309
N-glycosylation sites:	Amino acids 67-70;103-106;156-159; 183-186;197-200;283-286
cAMP- and cGMP-dependent protein kinase phosphorylation sites:	Amino acids 228-231;319-322
N-myristoylation site:	Amino acids 116-121
Amidation site:	Amino acids 488-491

10000157.031502

**FIGURE 13**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGGACAGAG  
AGTGACACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTCCAGCCCCCTGCCA  
CCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGGCAGCACAGGGCCTCAGGCCTGGGT  
GCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCTTGGCACTGGGCGAAGCCCAGTGG  
TCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTC  
TGGGACAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCA  
CCTGCAGACAGAGCTGGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC  
ACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGG  
GTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCC  
CTGCGTCTGTGCTGGAGGTGCAAGTGCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT  
GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTATACTCAGCCCAGGTACGAGAAGGA  
ACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACAACGTGCATC  
TGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCA  
AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTG  
CCTCTGTATTTCAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTCAGGGAGGACC  
CCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGAC  
GCACCGTGCTCGCTGCCCCGAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACT  
GGTCCCACCGCTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCACC  
CTAACCTCTGTGTTTCAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTG  
GGGECTCTCAAAGACGATGTGCTACTGTTGGAGACAGGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTT  
GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTAC  
TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCC  
ATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTC  
CCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGTGGCTGAGGCTCTTGAAACAGGACGTCCGCTCGG  
GGGCGGCCGCCAGGGGCCGCGCGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTG  
GGCGCCCTGGCGTGGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTGCTGAACT  
GAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCCAGACCCTGCAGGAGGGCGGCGTGGTGG  
TCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGG  
GCGCACGGCCCGCACGACGCCTTCCGCGCCTCGCTCAGCTGCGTGCTGCCCCACTTCTTGAGGGCCGGGC  
GCCCCGCAGCTACGTGGGGGCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGCA  
CCGTGCCCGTCTTCACTGCCCCCTCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCG  
CGTTCGGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACGCCAGCCCTGGATAGCTACTT  
CCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGACGGGA  
CTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

10000157 "031502"

14/71

FIGURE 14

MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAPTHLQTELV  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTFQAYPTARCVLLEV  
QVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSAAGDNVHLVNLVS  
EEQHFGLSLYWNQVQGPVKPRWHKNLTGPIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN  
LWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSAAAARG  
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFHQAQRQTLEGGVVVLLFSP  
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFT  
LPSQLPDFLGALQQPRAPRSGRLEQERAEQVSRALQPALDSYFHPGTPAPGRGVGPGAGPGAGDGT

signal sequence:	Amino acids 1-20
transmembrane domain:	Amino acids 453-473
N-glycosylation sites:	Amino acids 118-121;186-189;198-201; 211-214;238-241;248-251;334-337; 357-360;391-394
<hr/>	
Glycosaminoglycan attachment site:	Amino acids 583-586
cAMP- and cGMP-dependent protein kinase phosphorylation site:	Amino acids 552-555
N-myristoylation sites:	Amino acids 107-112;152-157;319-324; 438-443;516-521;612-617;692-697; 696-701;700-705

205757-031502

**FIGURE 15**

CGAGGGCTCCTGCTGGTACTGTGTTTCGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAGGCCATGCAG  
CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCATGGGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC  
TCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGCTTTCGCCACCTGCCCCACTGGAACACC  
CGCTGTCCTCTGGCCTCCACACGGATGACAGTTTCACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTG  
GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGC  
TGTCAAGGTGGCTCAGGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAAGTCTTCCACA  
TTCAAGTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTACCTGTCTC  
TGAGAAGAGCCATCACATTTCCATCCCTCCCCAGACATCTCCACAAGGGACTTCGCTCTAAAAGGACCC  
AACCTTCGGATCCAGAGACATGGGAAAGTCTTCCCAGATTGGACTCACAAGGCATGGAGGACCCGAGTTC  
TCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTGCGGTGACCATATCTTCAGGCCCTGAGGTGAGCGTGCG  
TCTTTGTCAACAGTGGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTG  
GGGGCCACACTGTAGAGCTGCCTTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAA  
GAGGACACTGTGAGGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAA  
GTCAGTGCACTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCCCACTGA  
AGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATAACCTTTGCAAAGACCTCCCGAATGCCACGGCT  
CGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCCCAGCTCTGCTTCAAGTTCTCTTT  
TGGAACAGCAGCCATGTTGAATGCCCCACCAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA  
CCCAAGCCCAGCAGCTGATTCTTCACTTCTCCTCAAGAATGCATGCCACCTTCAGTGCTGCCTGGAGCCTC  
CCAGGCTTGGGGCAGGACACTTTGGTGCCCCCGTGTACACTGTGAGCCAGGCCCGGGGCTCAAGCCCAGT  
GTCAGTAGACCTCATCATTCCCTTCCTGAGGCCAGGGTGCTGTGTCCTGGTGTGGCGGTGAGATGTCCAGT  
TTGCCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCACTGCTG  
GCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTCAGGCCCGGGGCCAGC  
GCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGCGCCTGGTGGGAGCGCTGGCTGAAC  
TGCTACGGGCAGCGCTGGGCGGCGGGCGGACGTGATCGTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGT  
GGGCCCGCTGCCGTGGCTCTGGGCGGCGGACGCGCGTAGCGGGAGCAGGGCACTGTGCTGCTGCTGT  
GGAGCGGCGCCGACCTTCGCCCGGTGAGCGGCCCGACCCCCGCGCCGCGCCCCCTGCTCGCCCTGCTCCAC  
GCTGCCCCGCGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC  
GCTGCGCGCCCTGCCGCGCTACCGCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGGACGCGCGGC  
CTTTCGAGAGGCCACCAGCTGGGGCCGCTTGGGGCGCGGCAGCGCAGGCAGAGCCGCTAGAGCTGTGC  
AGCCGGCTTGAACGAGAGGCCGCCGACTTGAGAGCTAGAGTTCAGGAGCTCCACCGCAGTCCCGGGTGTCT

205757 "031500"

FIGURE 16

MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFTGSSAYIPCRTWWALFSTKPWCV  
RVWHCSRCLCQHLLSGGSLQRGLFHLLVQKSKSSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISIPS  
PDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQWALECE  
ELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQH  
TQMVMALTLCPLKLEAALCQRHDWHTLCKDLNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPH  
QTGSLTSWNVSMQTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDLIIPFLR  
PGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLALLTLLGVVLALTCRRPQSGPGPARPVLLHAAD  
SEAQRRLVGALAELLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLLWSGADLRPVS  
GPDPRAPLLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYRLRLDLPRLLRALDARPF AEATSWGR  
LGARQRRQSRLELC SRLERE AARLADLG

Signal peptide:	Amino acids 1-23
Transmembrane domain:	Amino acids 455-472
N-glycosylation sites:	Amino acids 318-322;347-351;364-368
<hr/>	
Glycosaminoglycan attachment site:	Amino acids 482-486
cAMP- and cGMP-dependent protein kinase phosphorylation sites:	Amino acids 104-108;645-649
Tyrosine kinase phosphorylation site:	Amino acids 322-329
N-myristoylation sites:	Amino acids 90-96;358-364;470-476
Eukaryotic cobalamin-binding proteins:	Amino acids 453-462

205T50" 45T0000T

**FIGURE 17**

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGGAGTGGGGGAGGTGAGACGGGGCGGTTGGAGGGGGAGGGAT  
GCCACGCGCTTCTGCCTCAGGTGTTCCCTGCGTTGTTTGTGAGTGGAGAGCAGGGAGTGGGGCCAGCCAGCA  
GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAG  
CATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT  
TCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTGCGGTAATACTGGAGGAGCTGAAGT  
CGGAGGGAAGACAGTGCCAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAAGT  
GGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTTCGTAAAGGTTGTCCCTTTTCC  
TTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGC  
CGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC  
AGGTGTCCTTCGACCACGCACCCGATGGCTCGGACATGCAGGTGTCCTTCGACCACGCACCCGACAACCTTC  
GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGCA  
GGAGCAAACCTACAGAGATGACCAGCTGCCTCCTTCAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG  
TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACCTCCCGTGGGCCGGG  
CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGAT  
GTGCCGCAAGAAGCAACAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACA  
CTGCAGCACTCCCAAGAGAGAGGCTCCGGCCGCGGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGC  
CAGAATCACATGAATGTCGTCCAGTGTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCT  
GGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTCTATCCAGAAGATCCACGAGT  
CCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAA  
GGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTCTTCTGGTGGCGGTGTGAGCCATTGCCGAAAAGCTCCG  
CCAGGCCAAGCAGAGTTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGCTACTTTGATTATTCTTGCAGG  
GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTTCC  
CACCTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAACATA  
CTTCCGGAGCAAGTCAGGCCGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGC  
CCGACTGGTTGAAAAGCAGTTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGAG  
AAATTTGATTGCGGCTTGTTTAAATGATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAA  
GGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGGGGGCCTGG  
ACCAAGACGGGGAGGCCCGGCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAA  
GCCGGCAGCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTC  
TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCTCTCT  
CTTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCTTCCAAGCTCCTCTCTTCTGGGTGATGCAAAGCA  
GATCTTGGTTGCCGAGCTACACTGATGAATCCACGCGGTGCCCCCTTTGTAACAAAACGAAAGAGTCTA  
AGCATTGCCACTTTAAAAA

1000157.031502

FIGURE 18

MPRASASGV PALFVS GEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT  
ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF  
PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHGSDMQVSFDHAPHN  
FGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA  
GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKD  
GQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKH  
KGGGRGSGKGELFLVAVSAIAEKLQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLC  
SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEDWFEKQFVFPFHPPLRYREPVL  
EKFD SGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAALQPLLHTV  
KAGSPSDMPRDSGIYDSSVPSELPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSSGSCK  
ADLGCRSYTDELHAVAPL

Transmembrane domain:

Amino acids 283-307

N-glycosylation sites:

Amino acids 31-34;38-41;56-59;  
113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:

Amino acids 232-235

Tyrosine kinase phosphorylation sites: Amino acids 312-319;416-424

N-myristoylation site:

Amino acids 19-24;375-380;428-433;  
429-434;432-437;517-522;574-579;  
652-657;707-712

"20575" 03150

[illegible]

h-IL17	30	N P G C P N S E D K N F	P R T V M V N L	I H N R N T N T N P K	- - - - -	- - - - -	R S S D
h-IL17B	43	H Q V P L D L V S R M K	P Y A R M E E Y	E R N I E E M V A Q L R	N S S E L A Q R K C E V N L	Q L W M	
h-IL17C	51	L L A R G A K W G Q A L	P V A L V S S L	E A A S H R G R H E R P S	A T T Q C P V L R P E E V L E A D		
h-IL17D	36	E E L L E Q L Y G R L A A G V	L S A F H T L Q L G P R E Q A R N	A S C P A G G R P A D R R F R P P			
h-IL17E	36	W P S C C P S K G Q D T S E E	L L R W S T V P V P P L E P A R P N	R H P E S C R A S	- - -	- E D G P	
h-IL17F	38	H T F F Q K P E S C P P V P G G S M K	L D I G I N E N Q R V S	- - - - -	- - - - -	- M S R N	

h-IL17  
h-IL17B  
h-IL17C  
h-IL17D  
h-IL17E  
h-IL17F

h-IL17	115	I Q E I L V L R R E . . . . .	P P H C P N S F R L E K I L V S V G C T C V T P I V H H V A
h-IL17B	143	V F S Q V P V R R L C P P P . . . . .	P R T G P C R Q R A V M E T I A V G C T C I F . . . . .
h-IL17C	151	L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V L P R S V . . .	
h-IL17D	136	V Y M P T V V L R R T P A C A G . . . . .	G R S V Y T E A Y V T I P V G C T C V P E P E K D A D
h-IL17E	132	L L Y H N Q T V F Y R R P C H G E K . . . . .	G T H K G Y C L E R R L Y R V S L A C V C V R P R V M G . . .
h-IL17F	123	I Q Q E T L V V R R K . . . . .	H Q G C S V S F Q L E K V L V T V G C T C V T P V I H H V Q

h-IL17D 179 SINSSIDKQGAKLLLGPNDA P A G P X

**FIG. 19**

Tissue	IL17D Distribution (approx.)
SPLEEN	120,000
BRAIN	120,000
SPINE	120,000
STOMACH	120,000
HEART	120,000
PLACENTA	120,000
THYMUS	120,000
KIDNEY	120,000
ADRENAL	120,000
PROSTATE	120,000
LIVER	120,000
PANCREAS	120,000
MUSCLE	120,000
LUNG	120,000
SALIVARY	120,000
TESTIS	120,000
COLON	120,000
TRACHEA	120,000
UTERUS	120,000
MARROW	120,000
MAMMARY	120,000
FETBRAIN	120,000
INTEST	120,000

FIG. 20

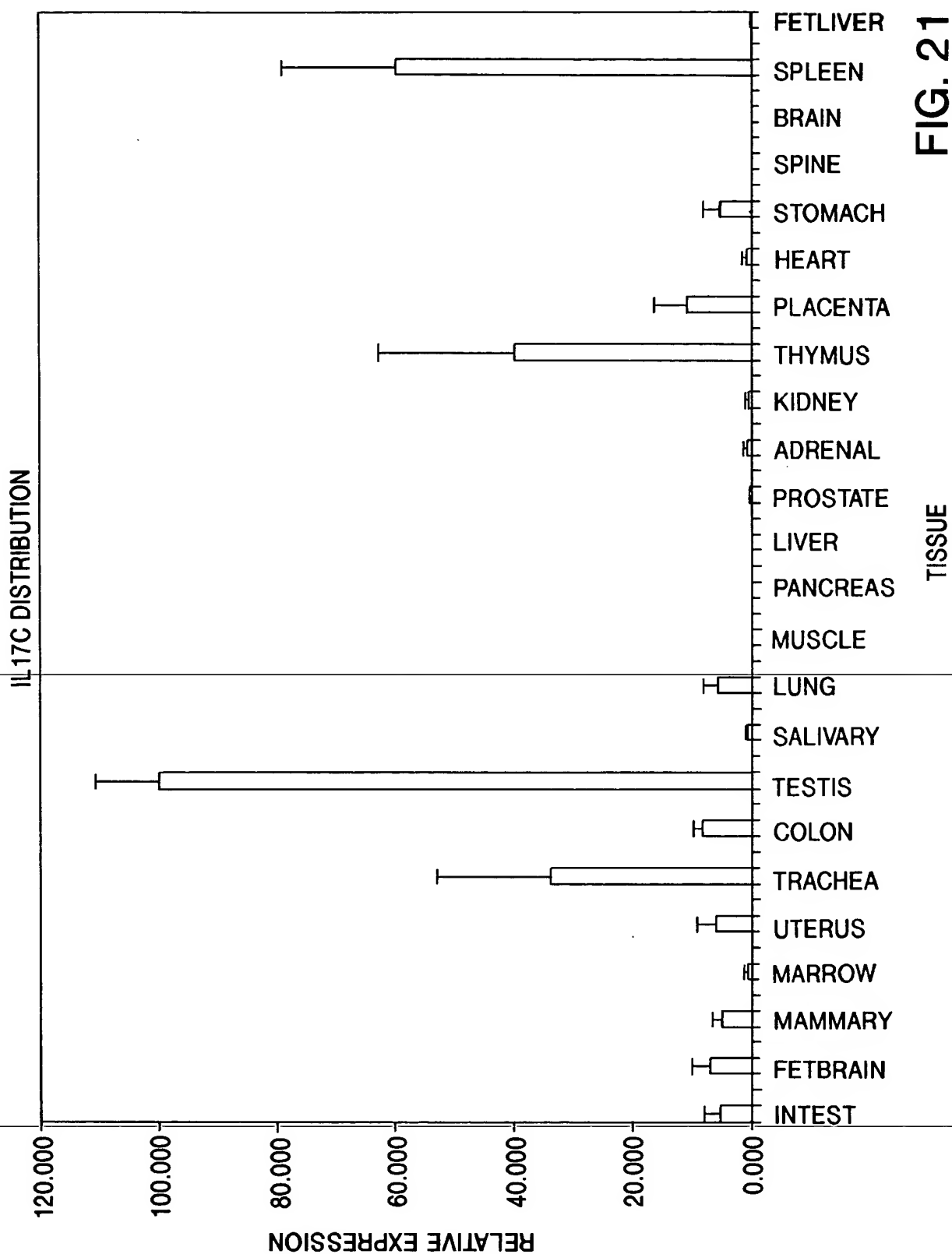
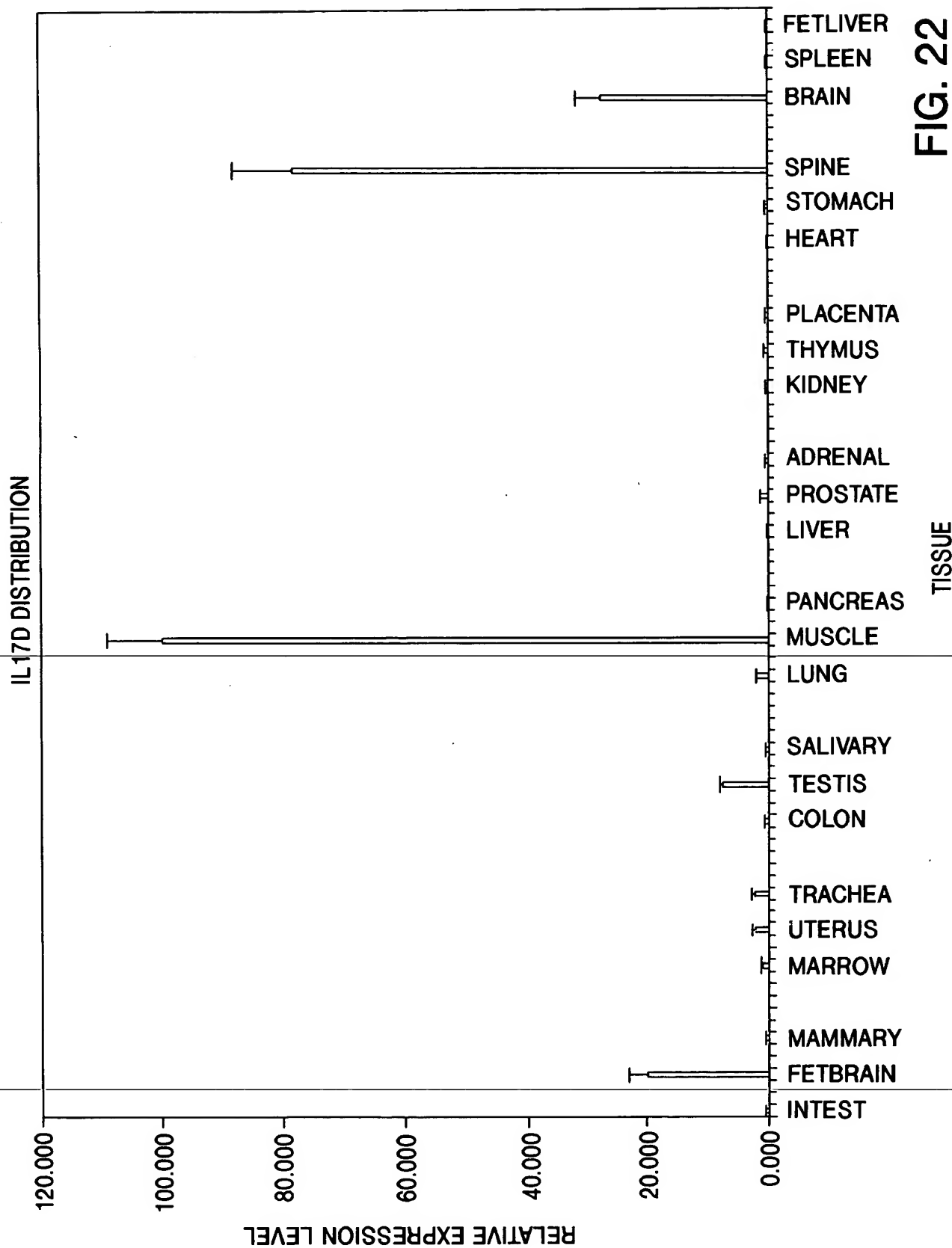


FIG. 21



**FIG. 22**

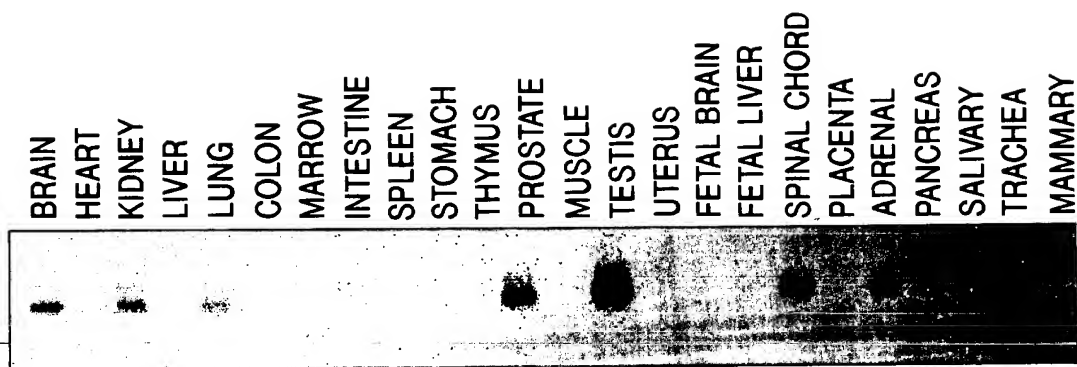


FIG. 23

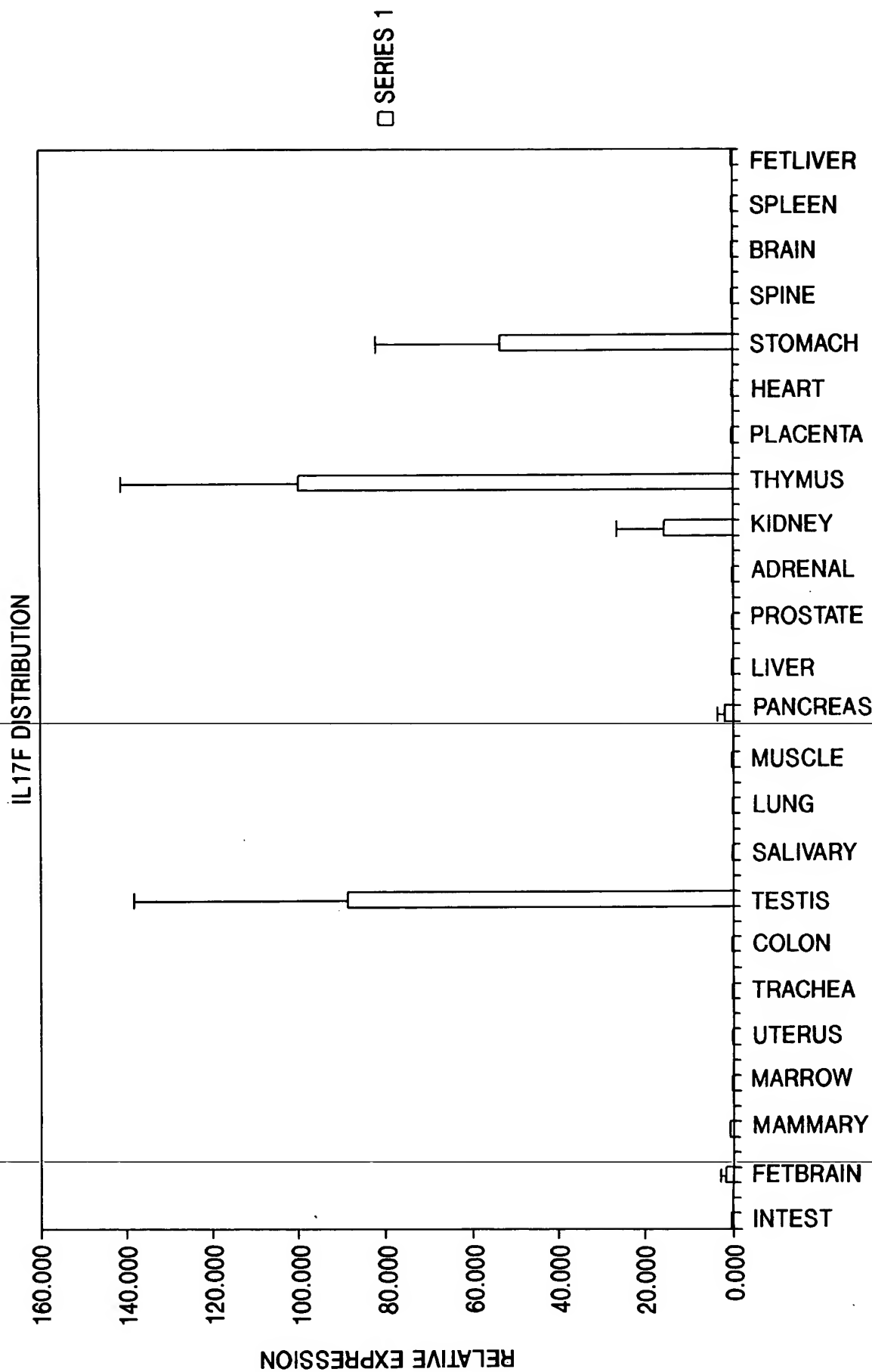


FIG. 24

IL17Rhom-1 DISTRIBUTION

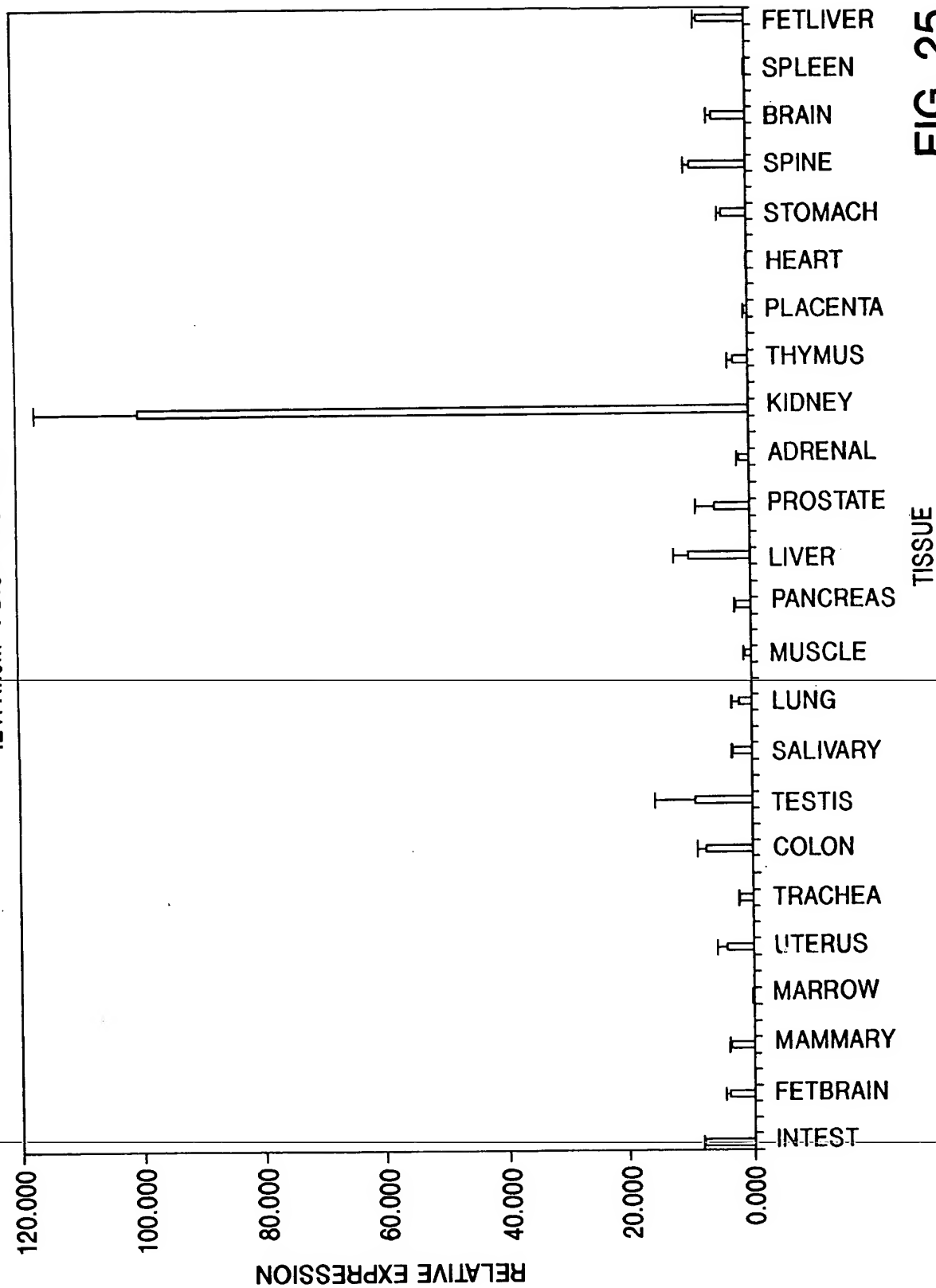


FIG. 25

200507 25100001

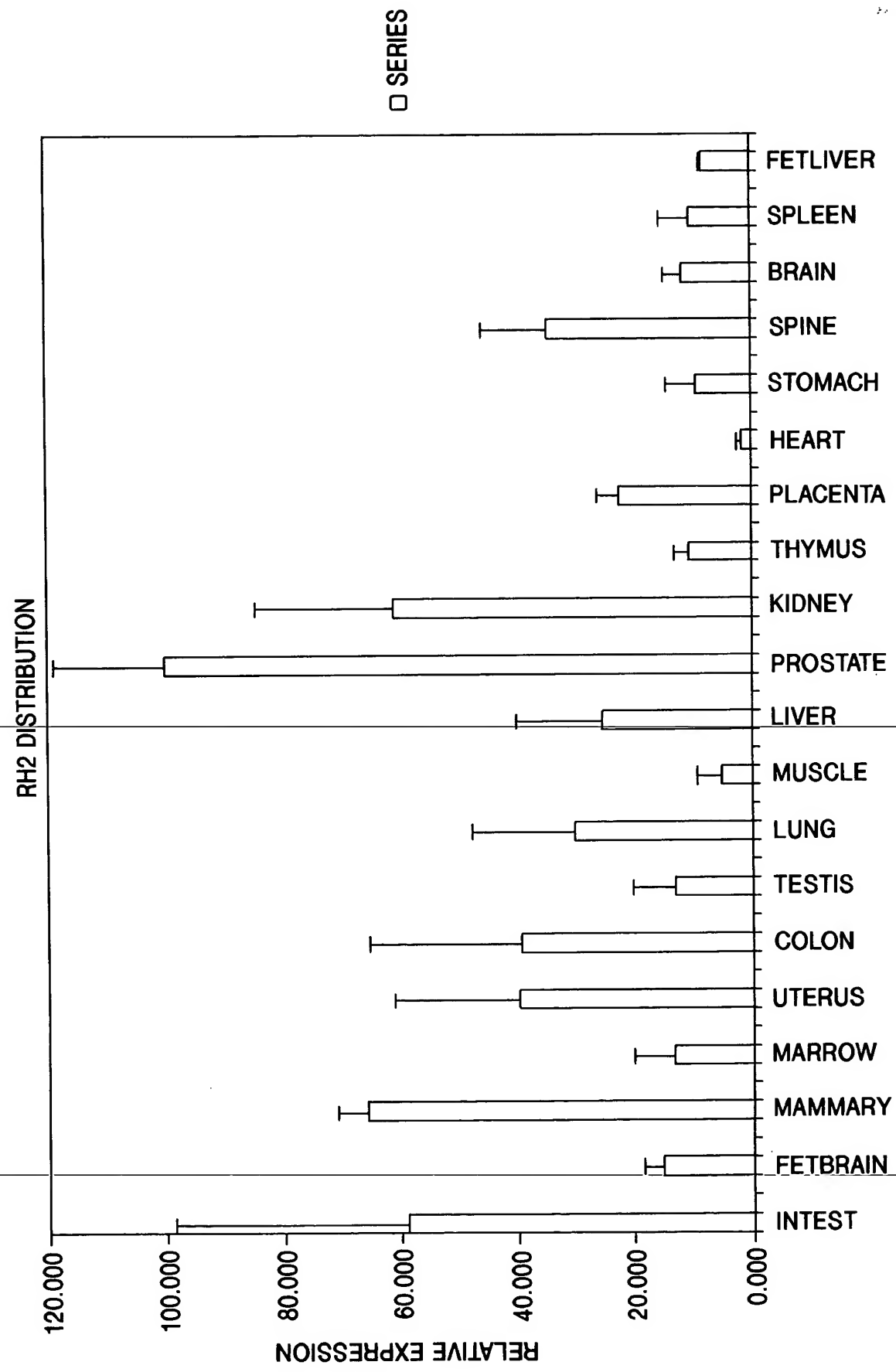


FIG. 26

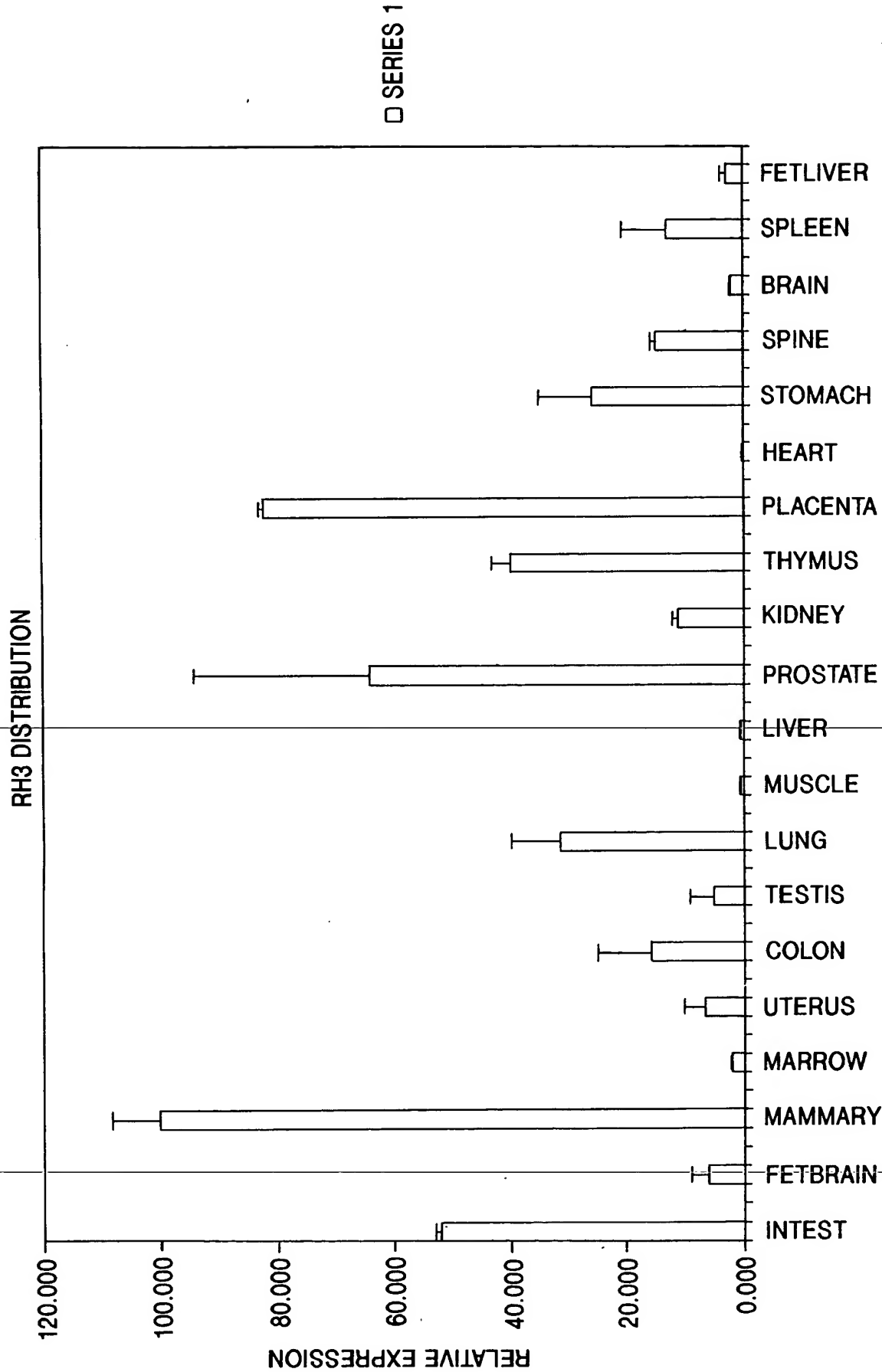


FIG. 27

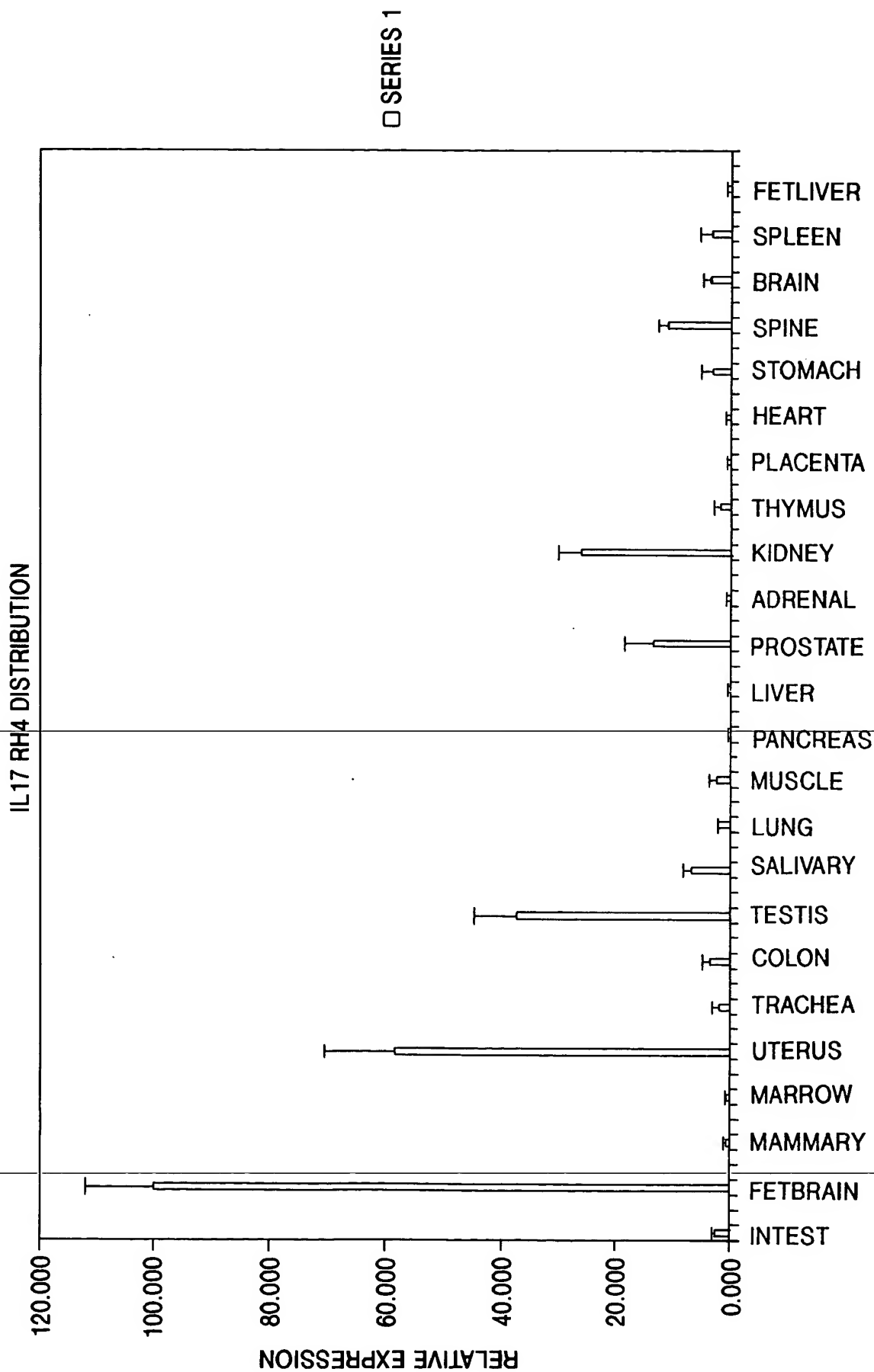


FIG. 28

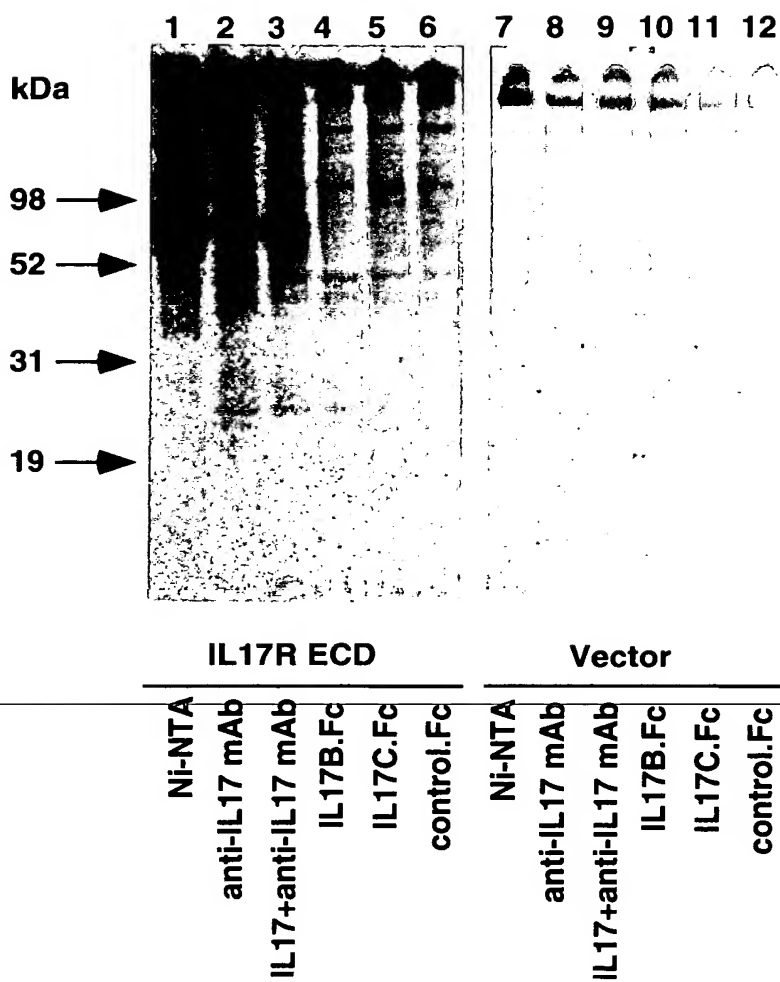


FIG. 29A

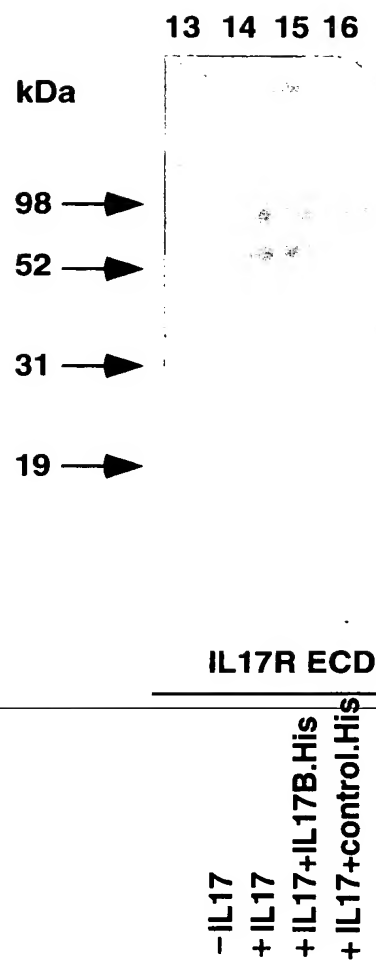


FIG. 29B

**FIG. 30**

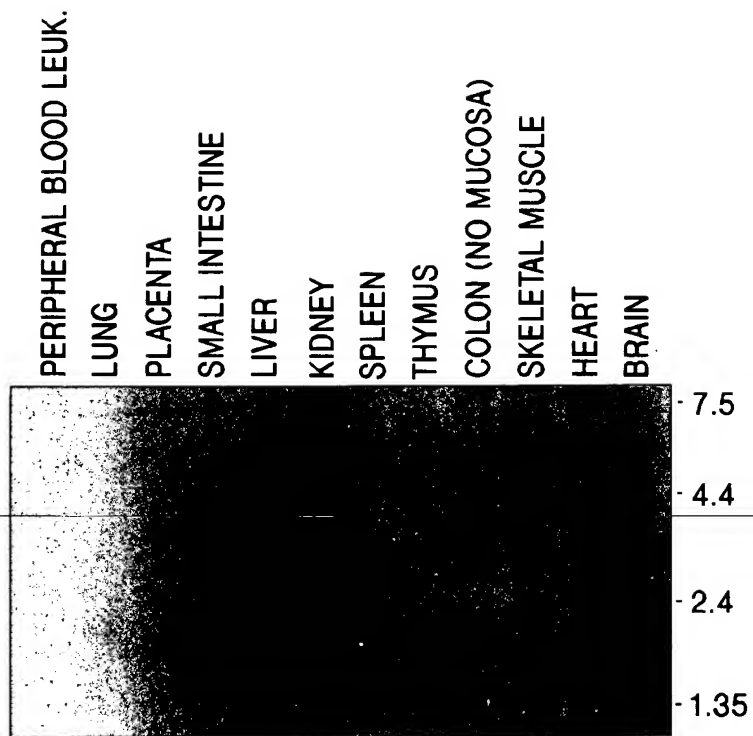


FIG. 31A

1000057.034502

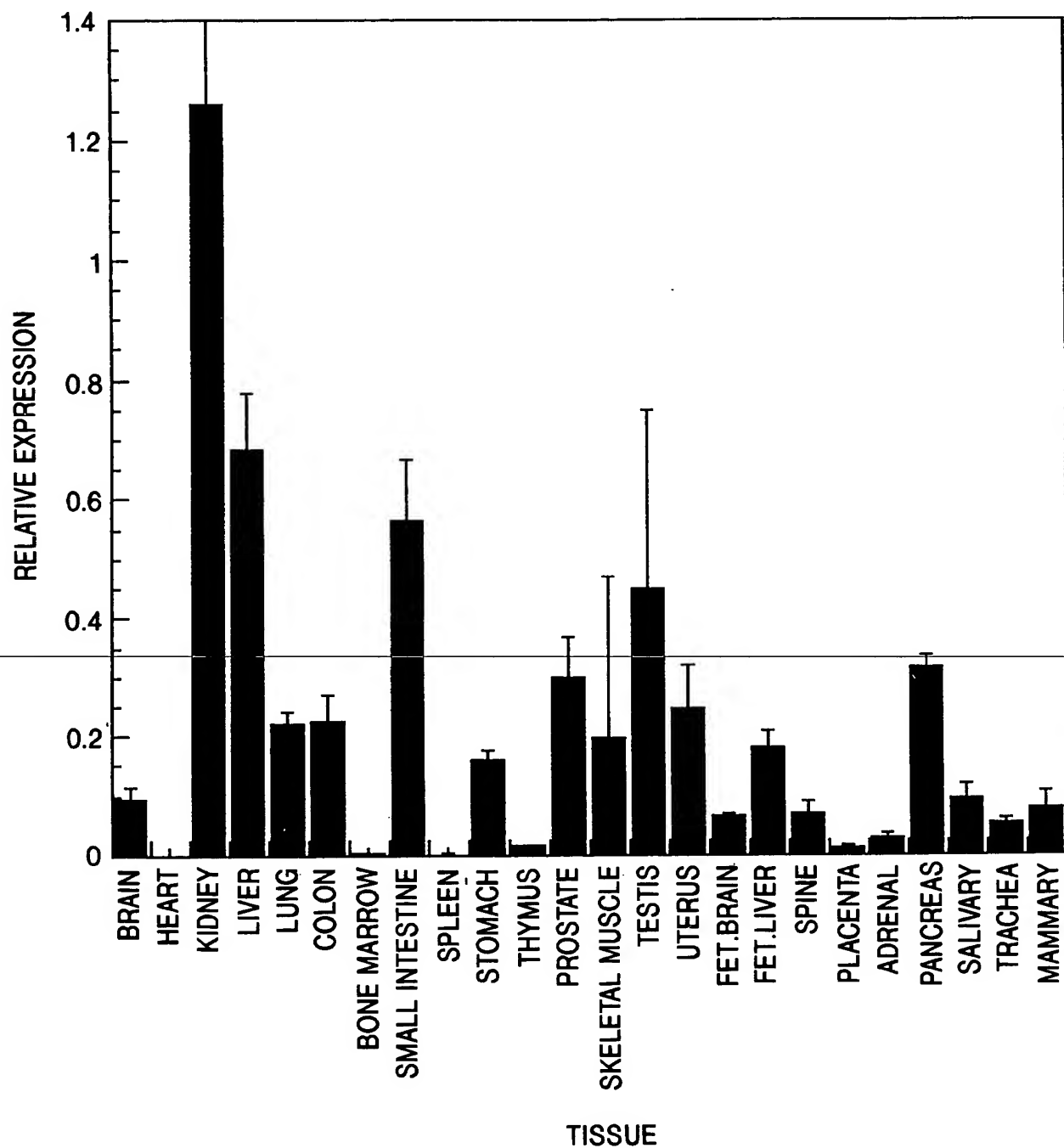


FIG. 31B

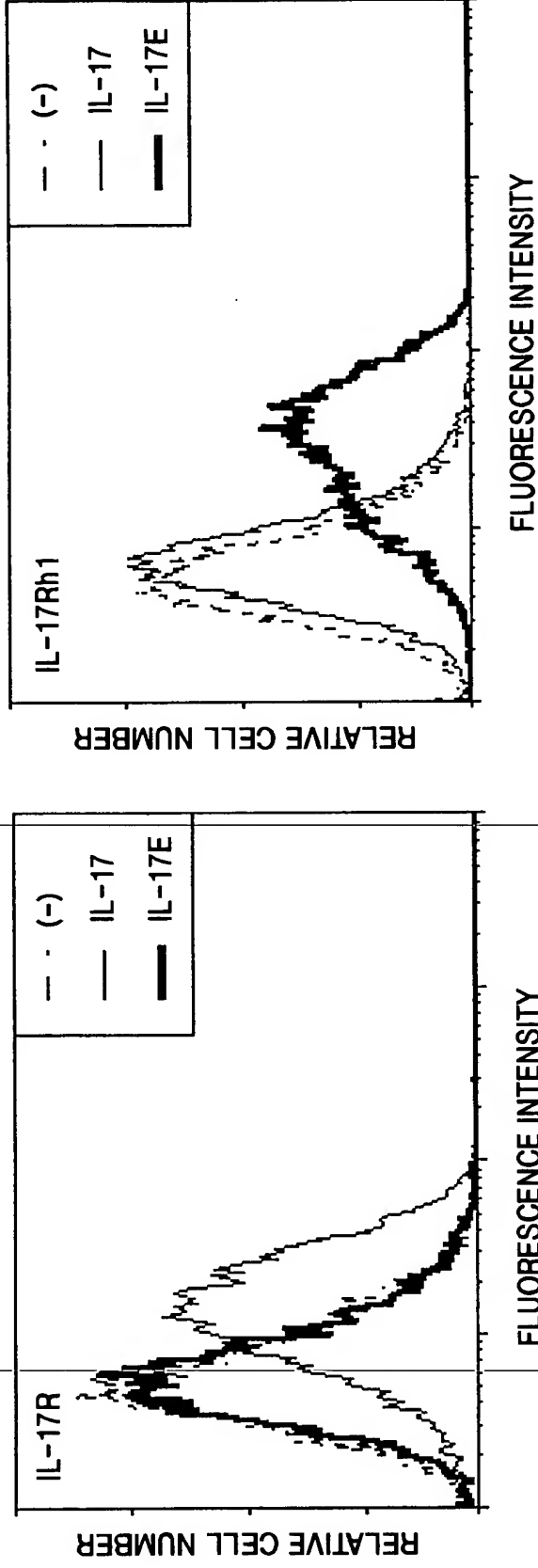


FIG. 32A



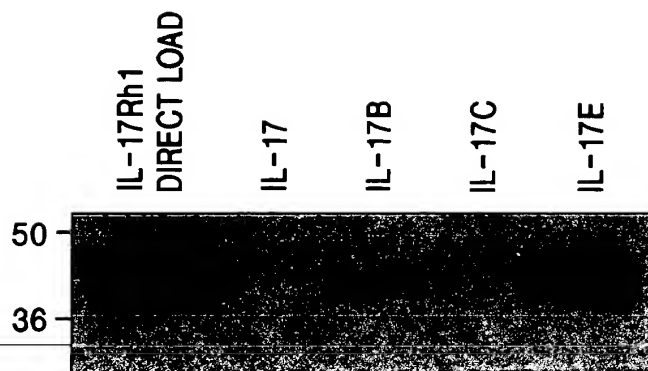


FIG. 32B

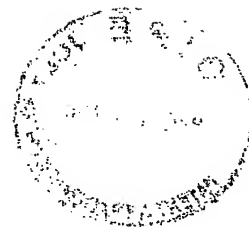




FIG. 33A

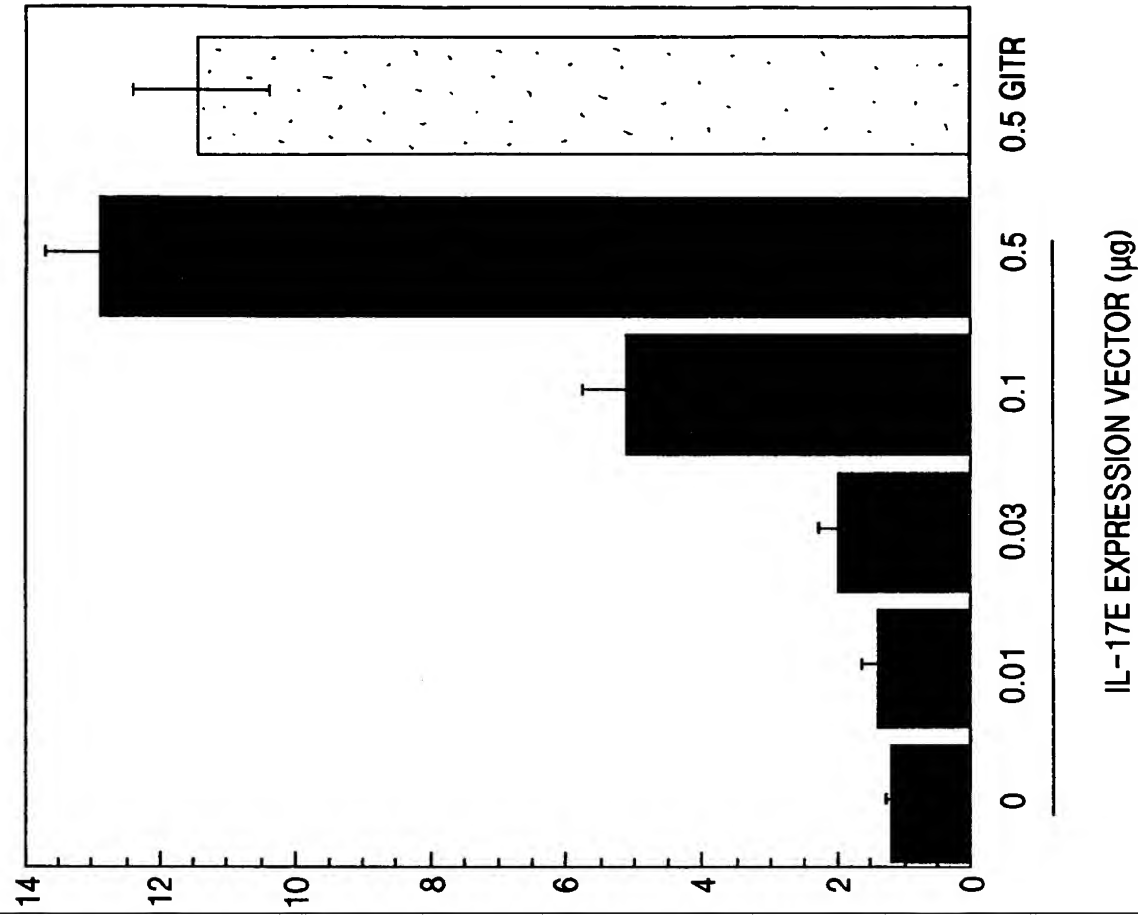


FIG. 33B

10000157-031502

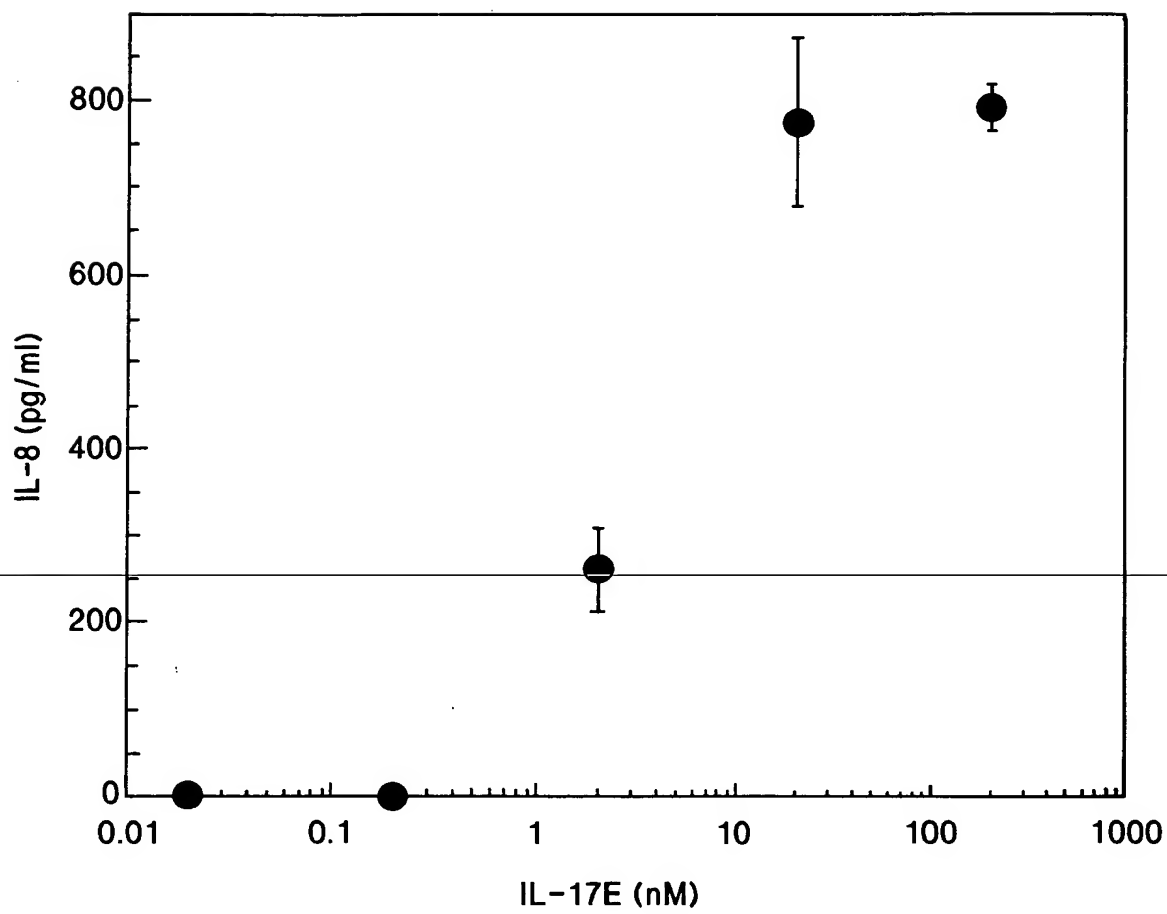
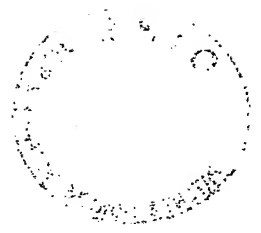


FIG. 34



IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN  
OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES

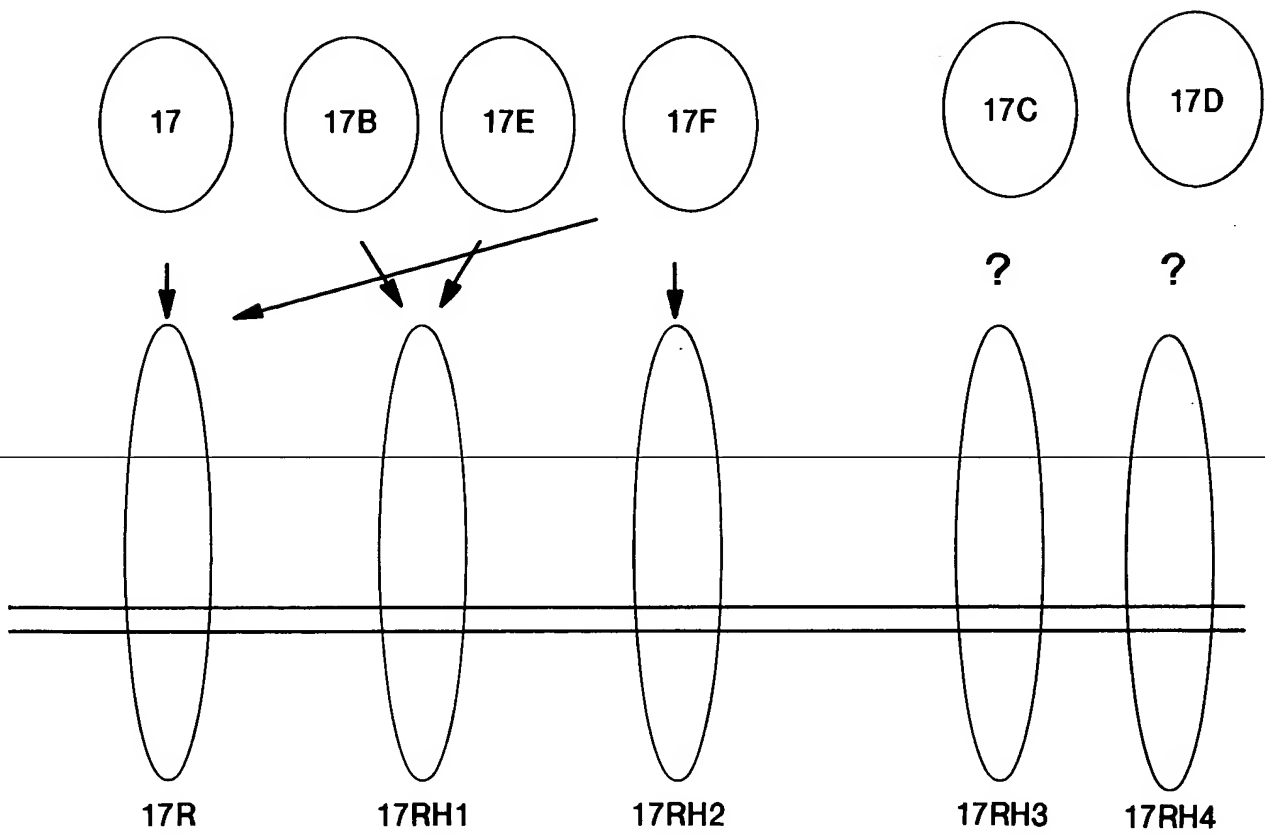


FIG. 35

10000157-52450

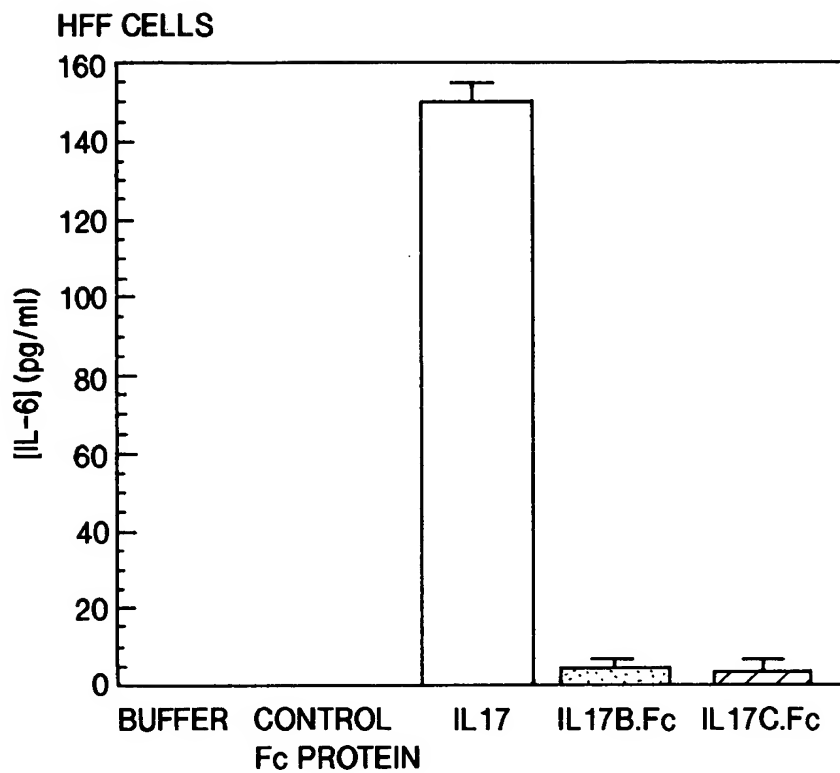


FIG. 36A

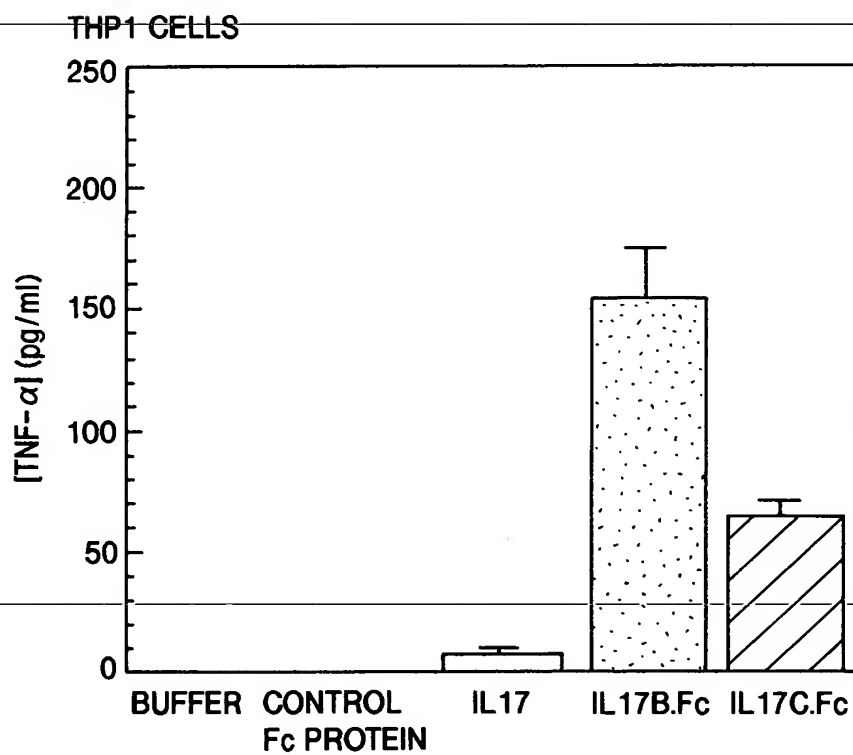
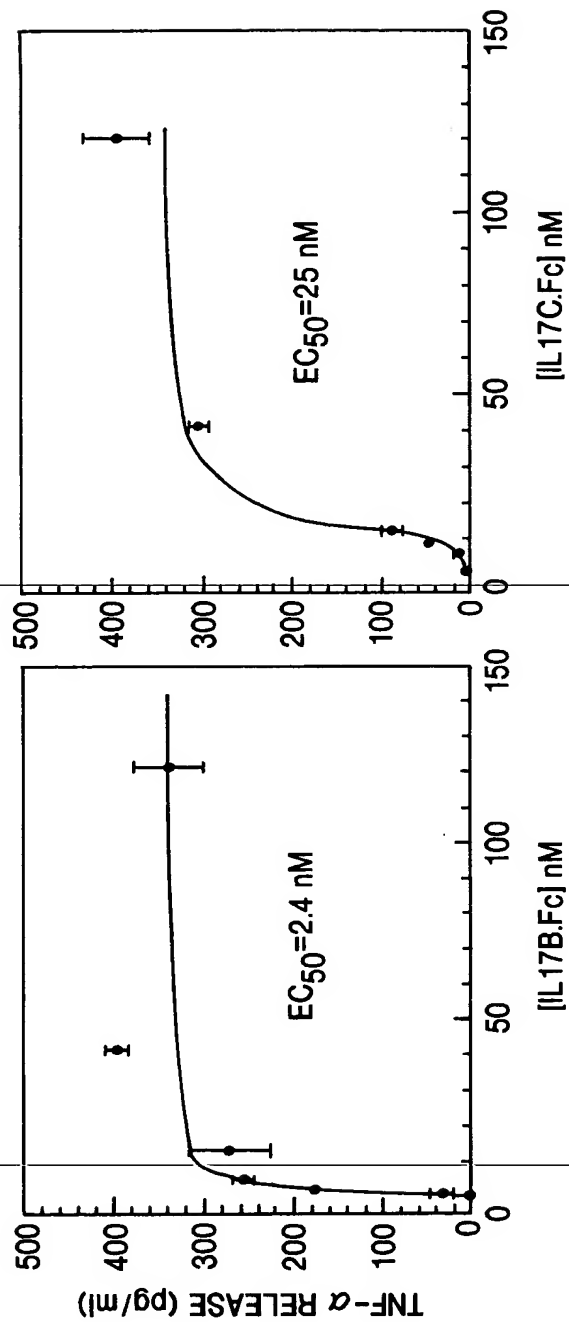
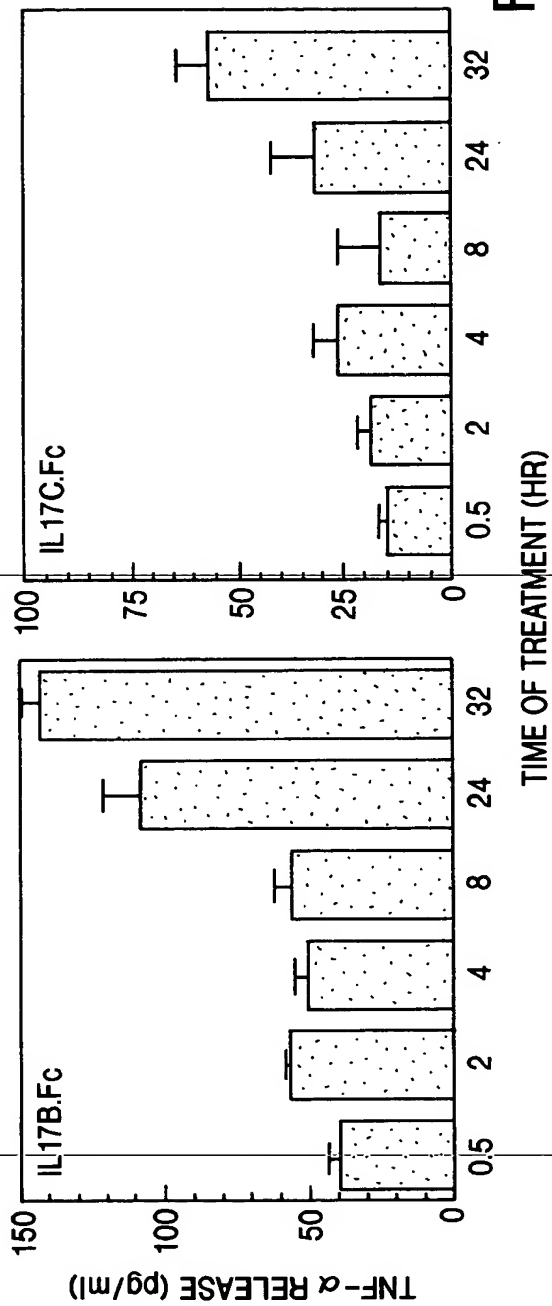


FIG. 36B



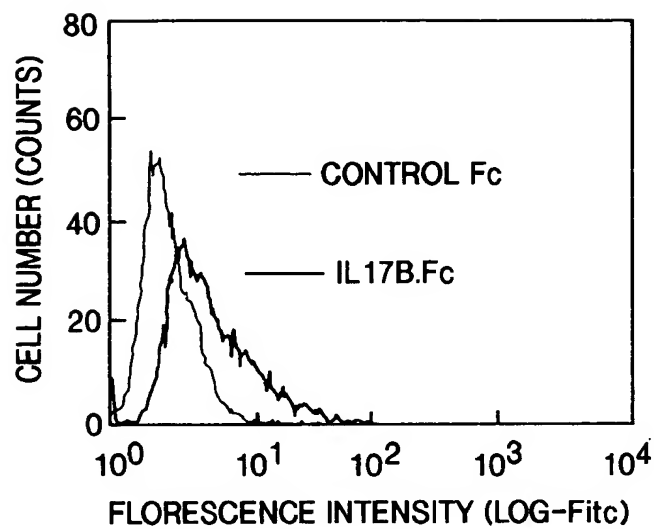


FIG. 38A

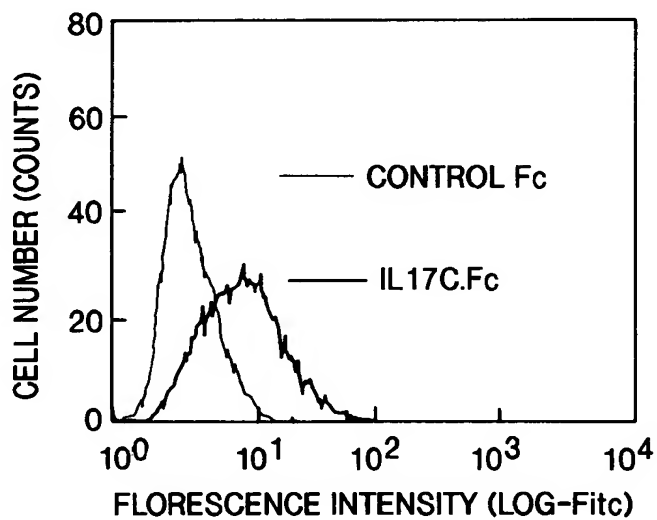
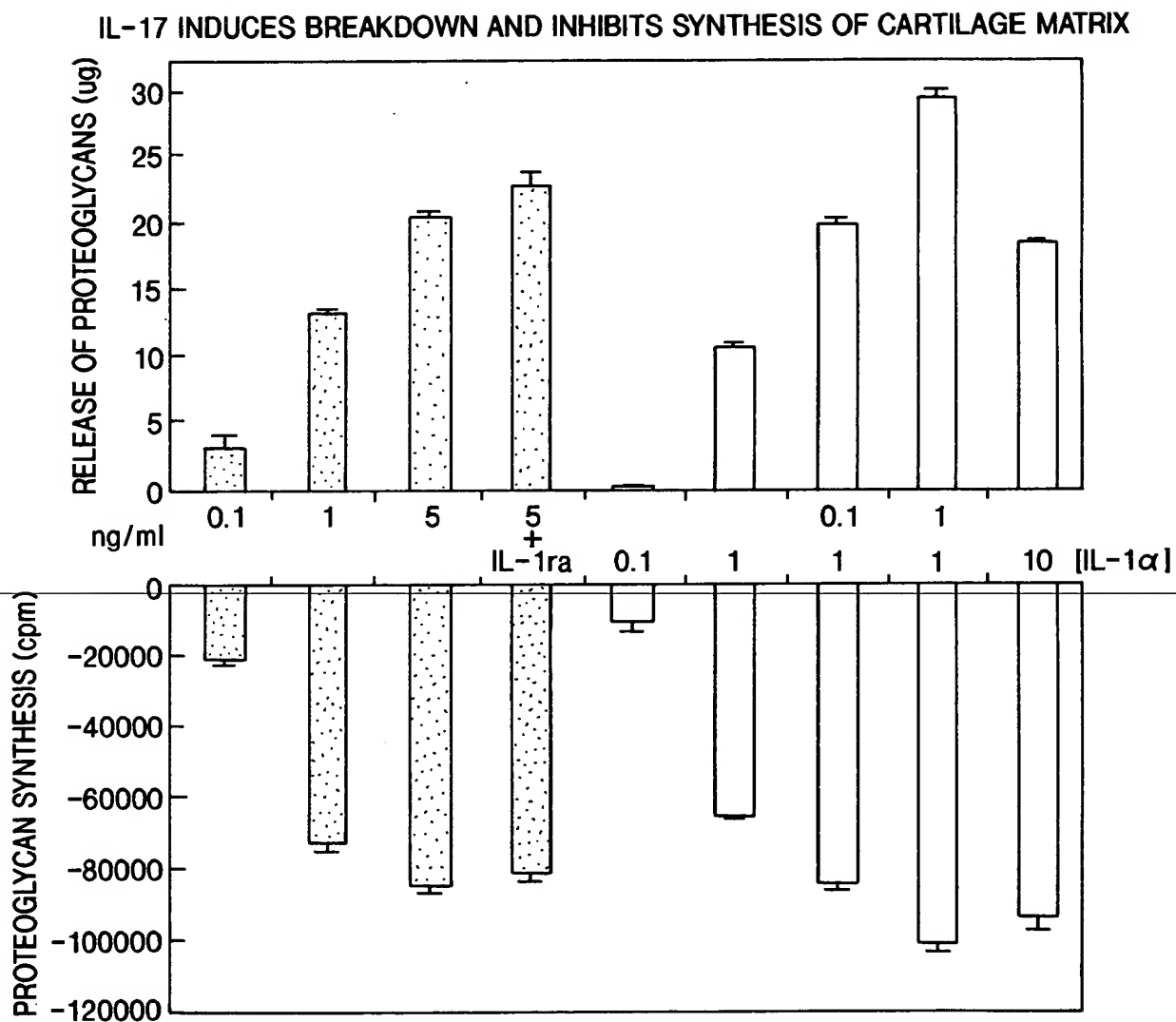


FIG. 38B



**FIG. 39**

IL-17 INCREASES BASAL AND IL-1 $\alpha$  -INDUCED NITRIC OXIDE RELEASE

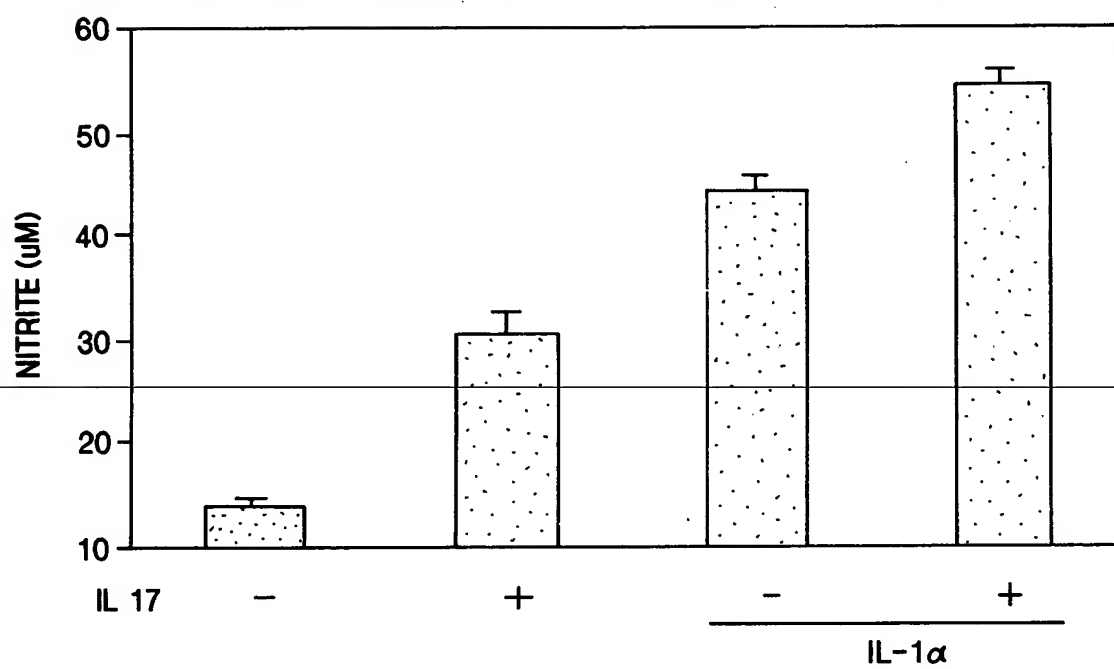


FIG. 40

INHIBITION OF NITRIC OXIDE RELEASE DOES NOT BLOCK THE DETRIMENTAL  
EFFECTS OF IL 17 ON MATRIX BREAKDOWN OR SYNTHESIS

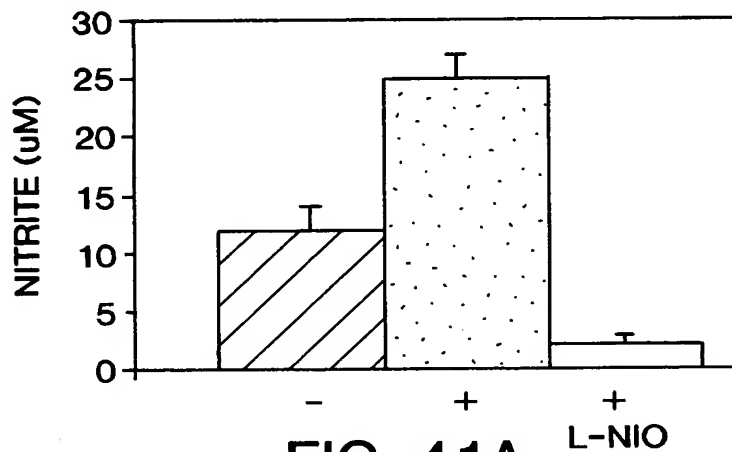


FIG. 41A

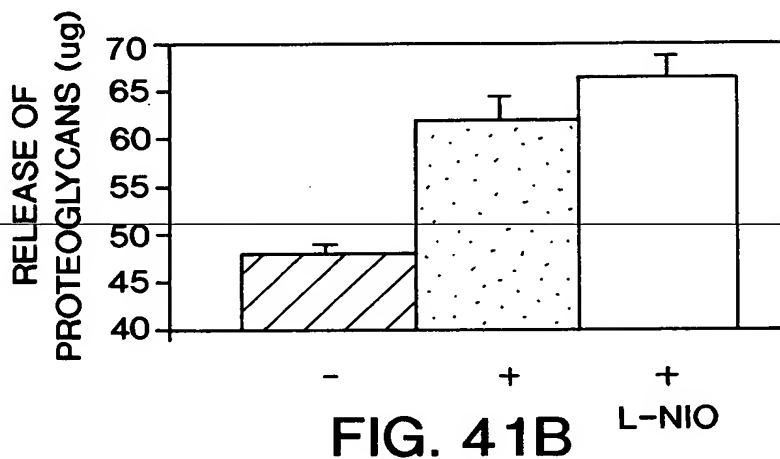


FIG. 41B

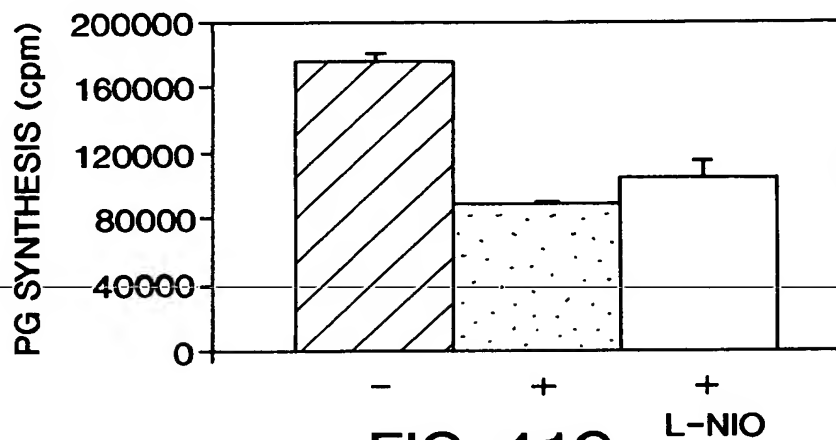


FIG. 41C

20070425T0001 10000157 034500

INHIBITION OF NO RELEASE ENHANCES IL1- $\alpha$ -INDUCED  
MATRIX BREAKDOWN BUT NOT MATRIX SYNTHESIS

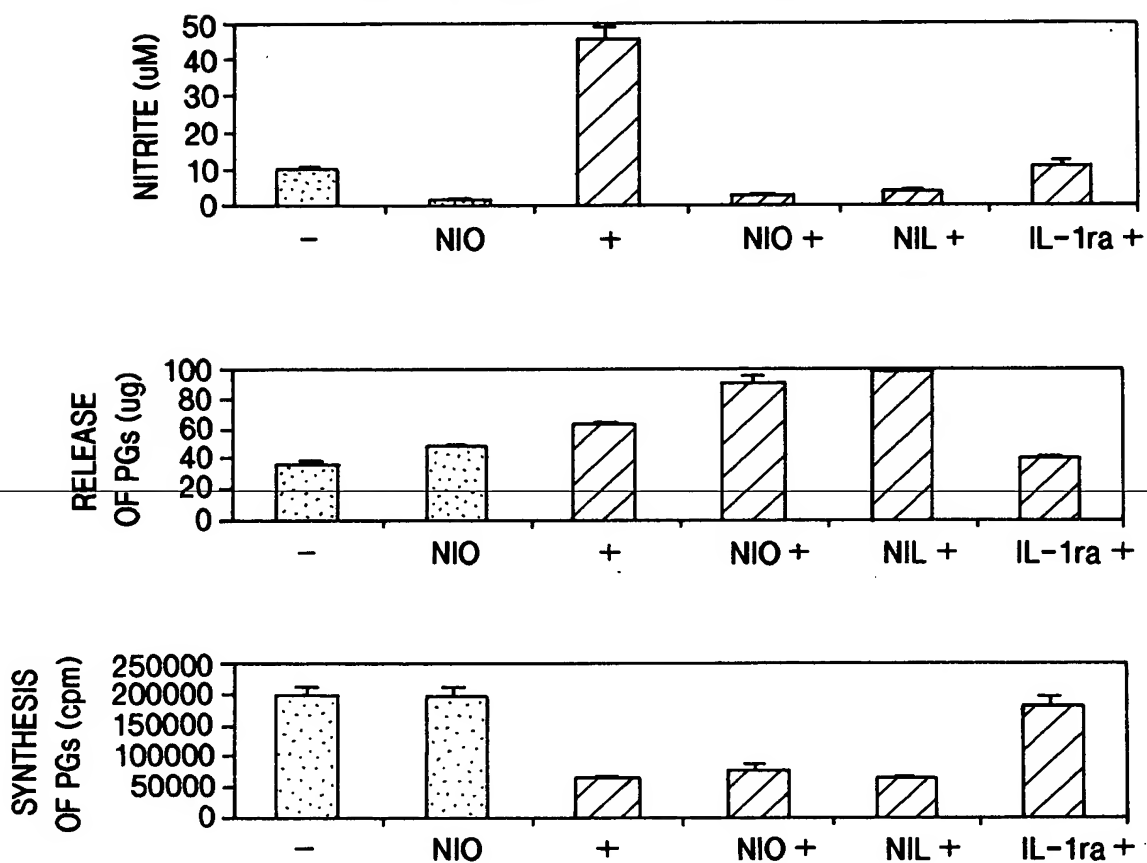


FIG. 42

# IL-17C DETRIMENTAL EFFECTS ON ARTICULAR CARTILAGE

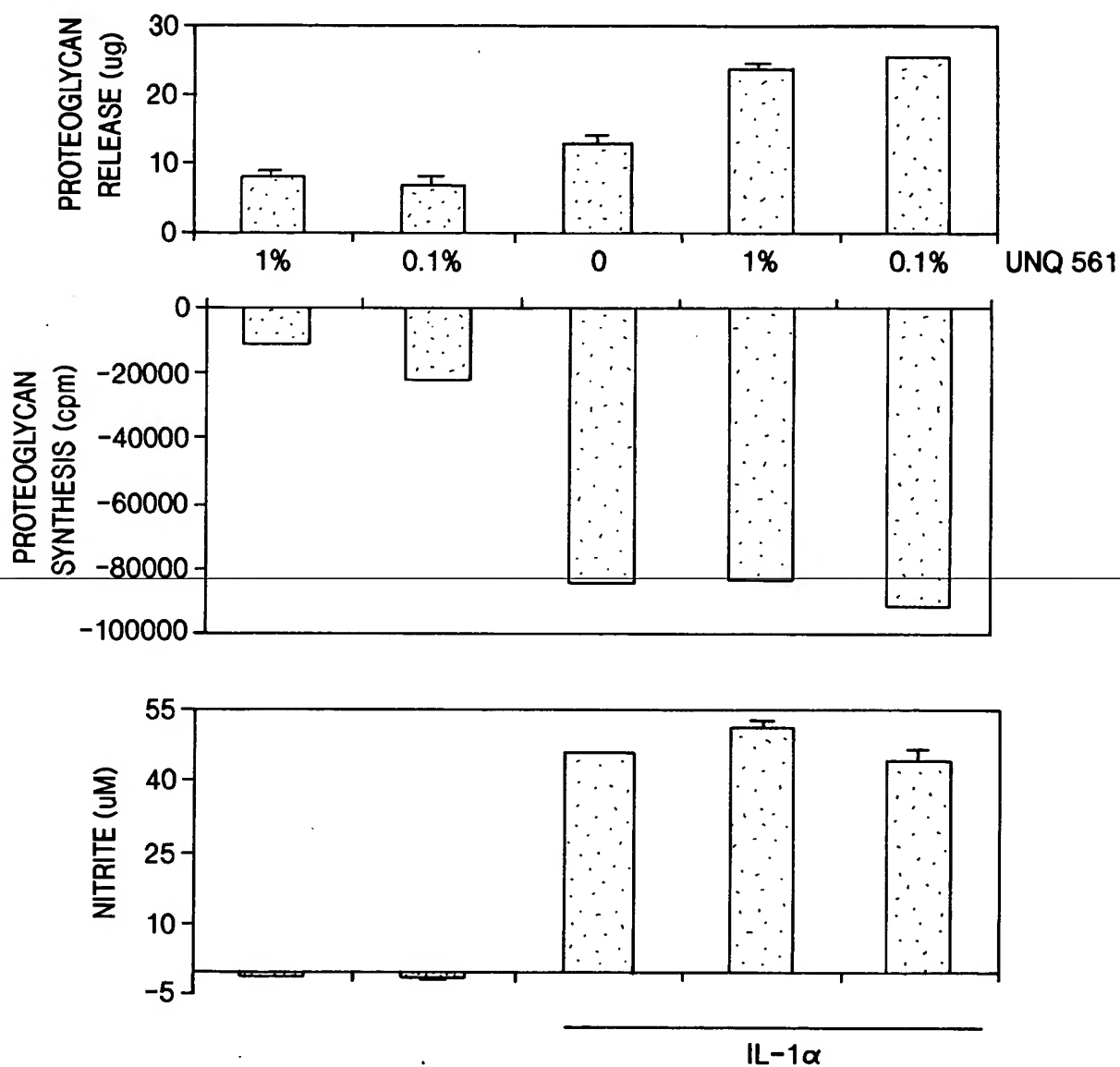


FIG. 43

INFLAMMATORY BOWEL DISEASE:  
EXPRESSION OF IL-17 FAMILY IN MOUSE MODEL OF IBD

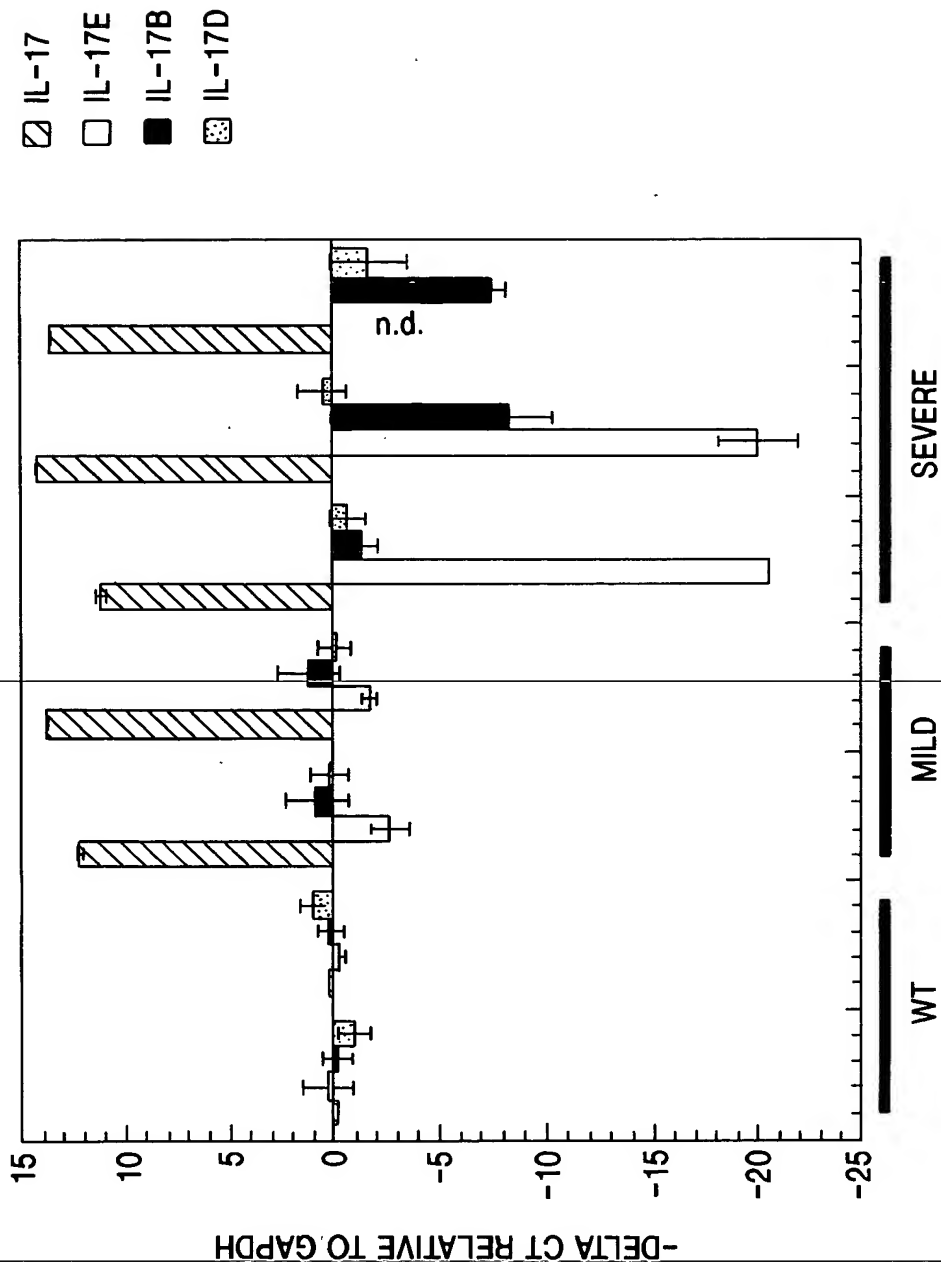


FIG. 44

IL-17D, PRESENT IN BRAIN, DECREASES RAPIDLY FOLLOWING STROKE

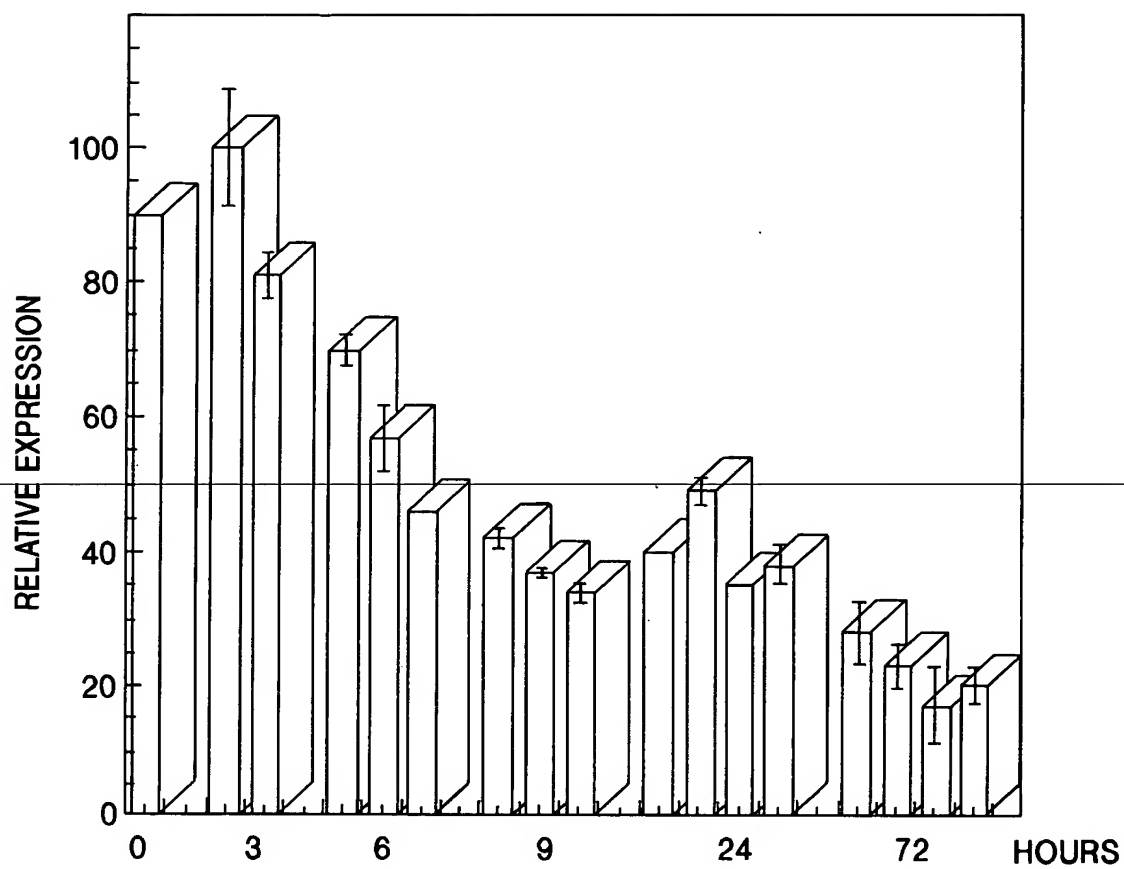


FIG. 45

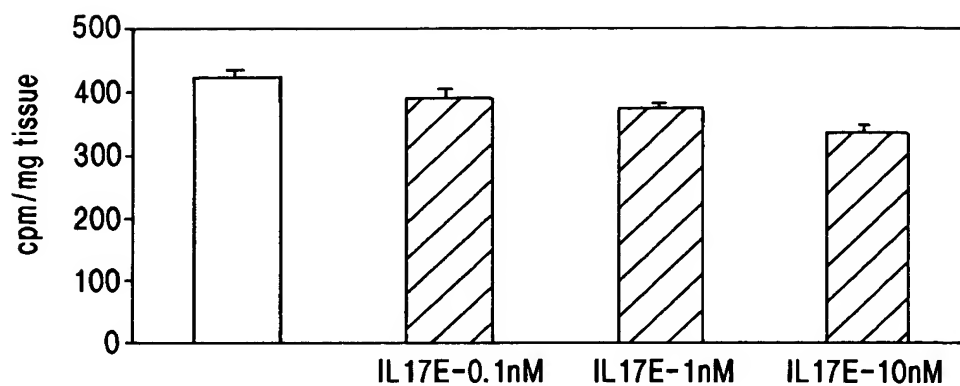


FIG. 46A

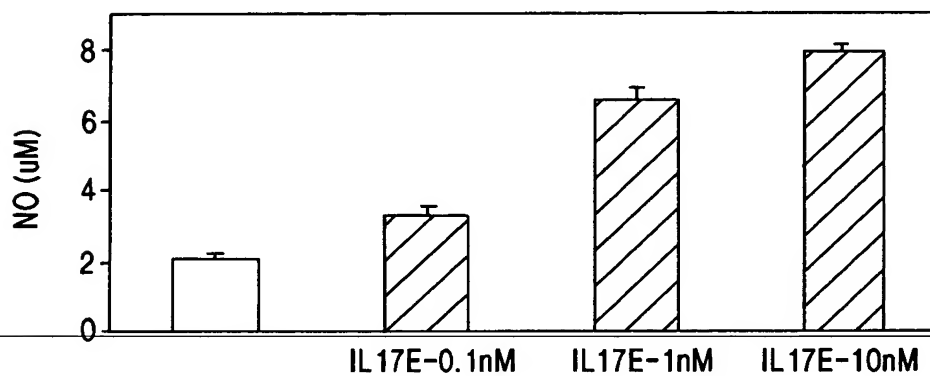


FIG. 46B

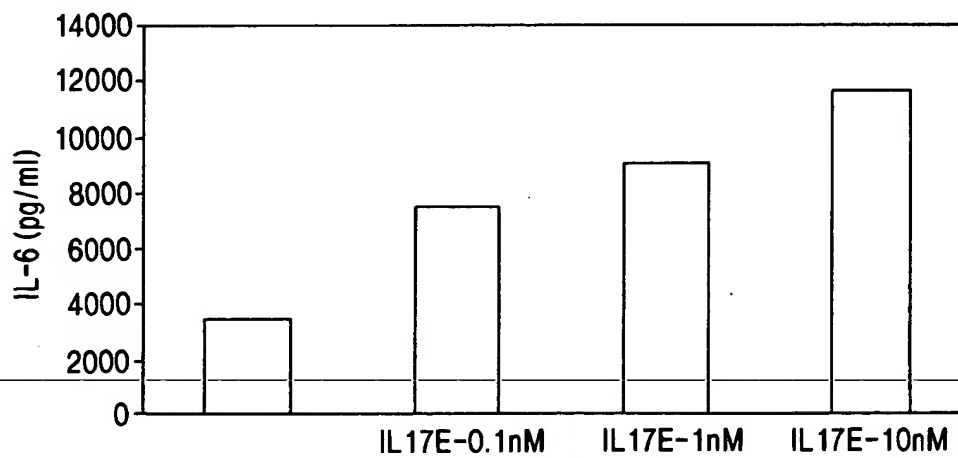


FIG. 46C

1000037.034500T

FIG. 47A

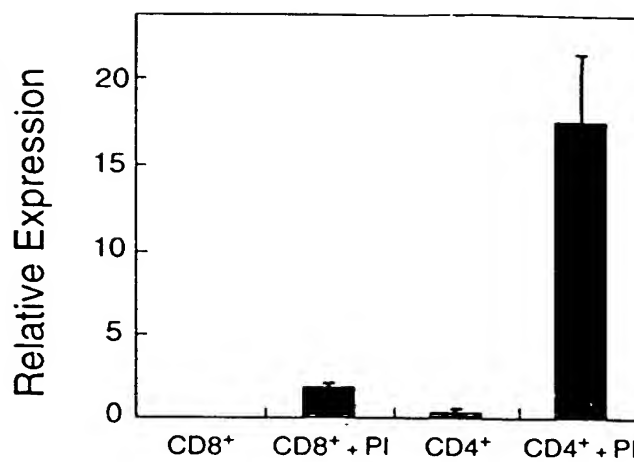


FIG. 47B

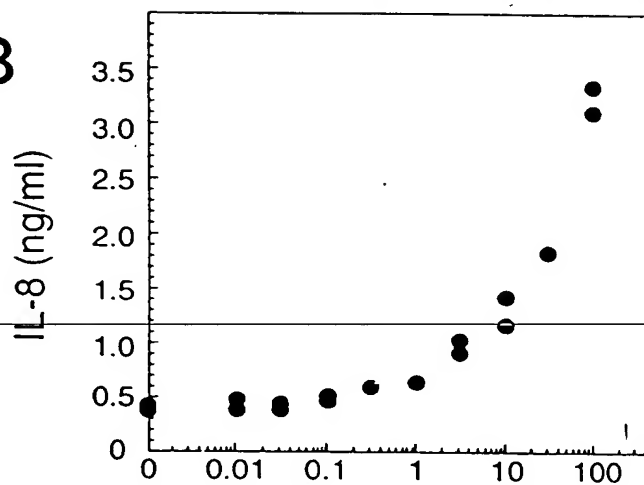
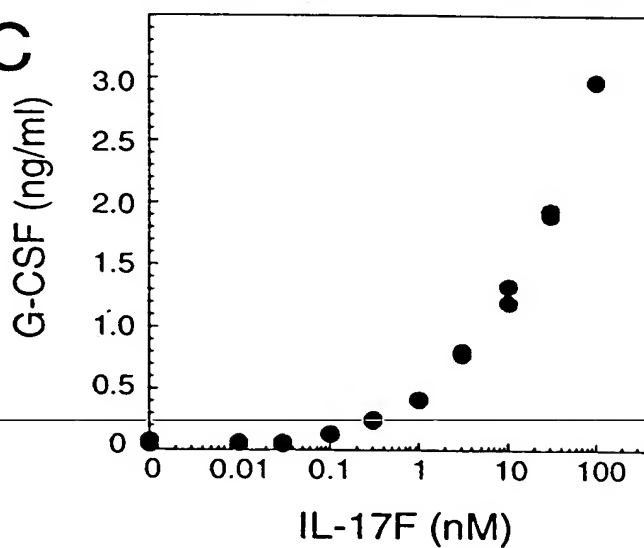


FIG. 47C



10000157.034502  
2004E0 25700007

## Porcine

Matrix  
Breakdown

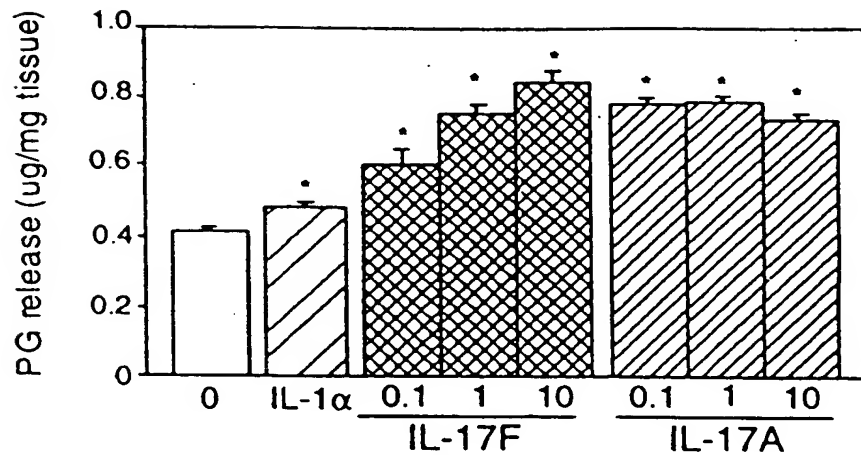


FIG. 48A

Matrix  
Synthesis

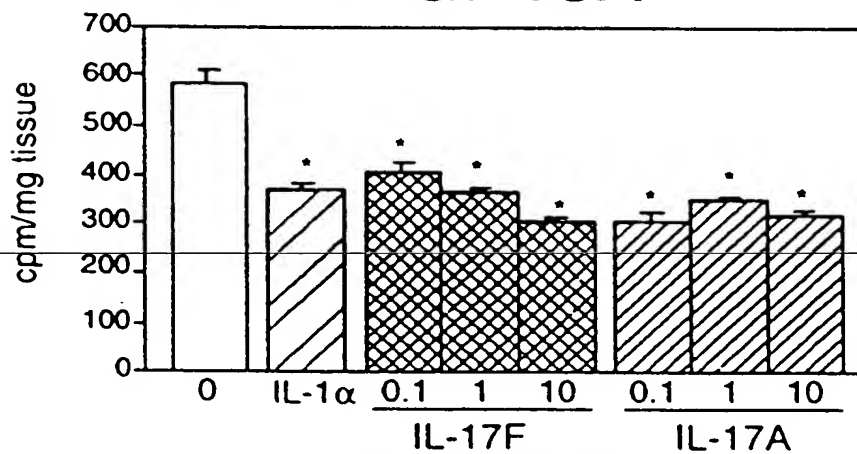


FIG. 48B

IL-6  
production

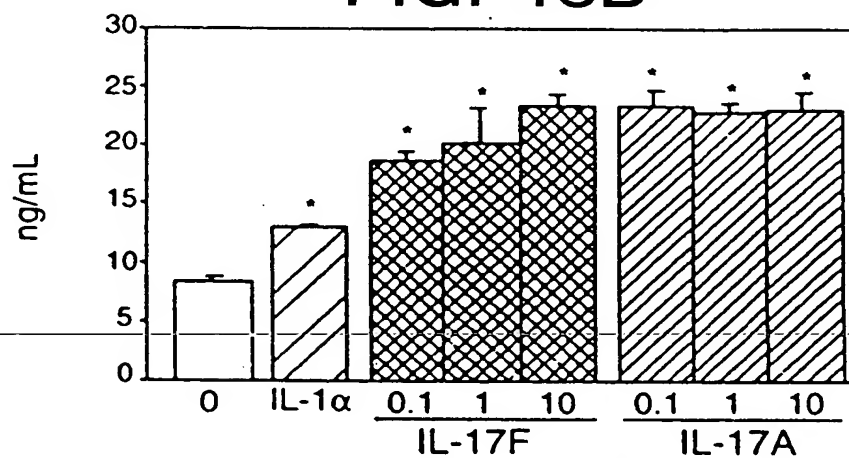


FIG. 48C

20050725T0001

# Human

Matrix Breakdown

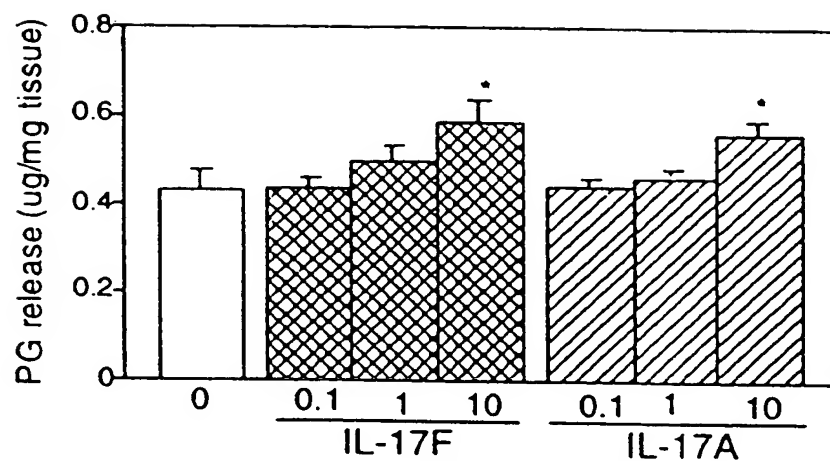


FIG. 48D

Matrix Synthesis

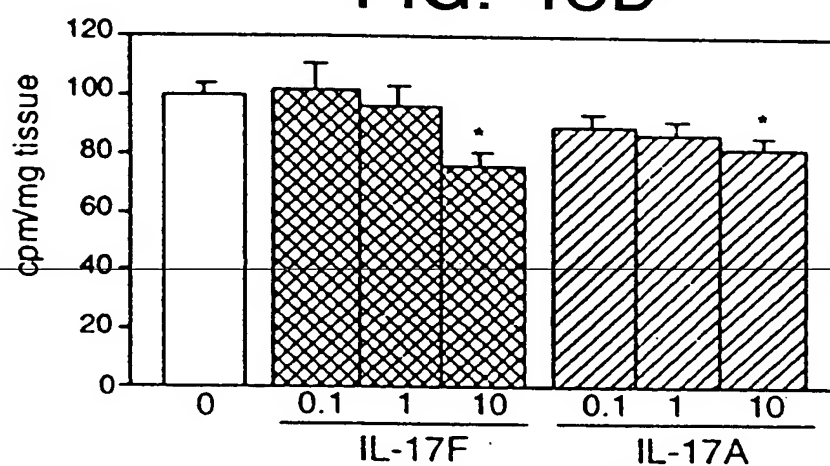


FIG. 48E

IL-6 production

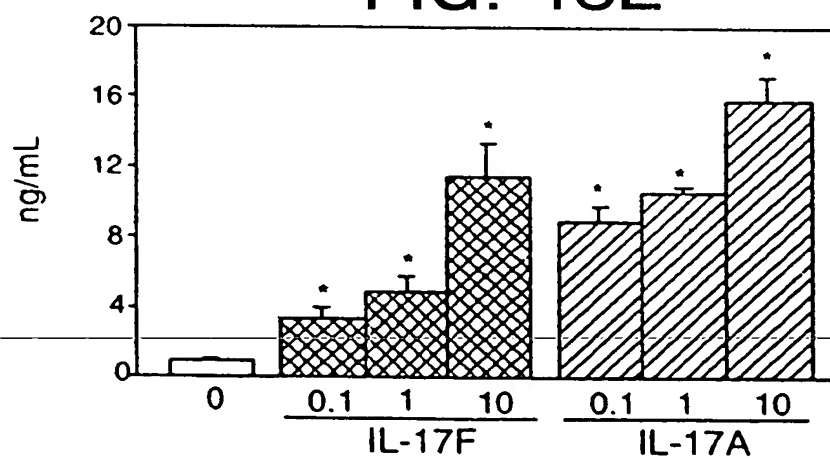


FIG. 48F

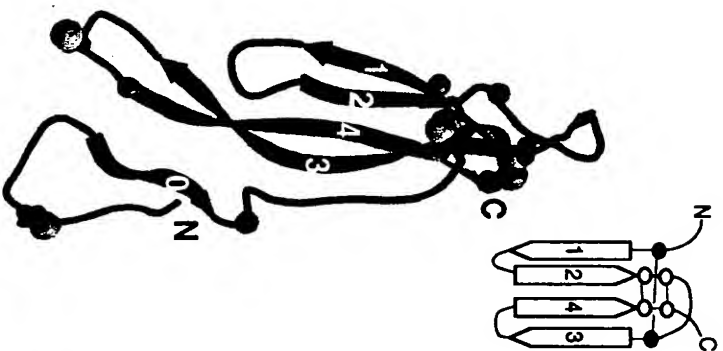


FIG. 49A

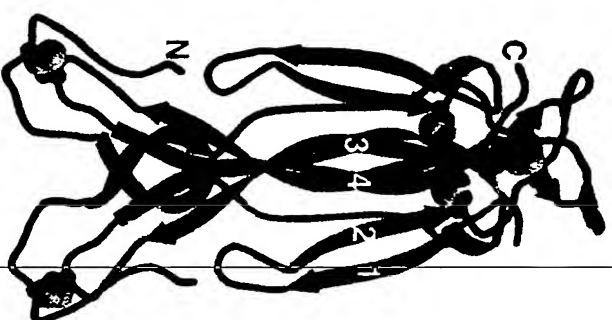


FIG. 49B

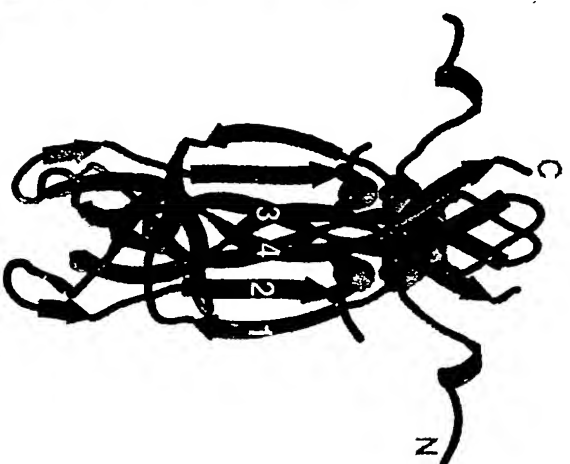


FIG. 49C

\*

IL-17F	.....	.....	.....	...RKIPKVG	HTFFQKPES	17
IL-17A	.....	.....	.....	.....IVKAG	ITIPRNP.G	14
IL-17B	.....QPRS	PKSKRKQGR	PGPLAPGPHQ	VPLDLVSRMK	PYARMEEYER	44
IL-17C	HHDP SLRGHP	HSHTGTPHYS	AEELPLGQAP	PHLLARGAKW	GQALPVALVS	50
IL-17E	.....	.....	.....YS	HWPSGCP SKG	QDTSEELLRW	22

0

IL-17F	PPVPGG....	....SMKLDI	GIINENQ RVS	MSRNIESRST	PWNYTVTWD	59
IL-17A	PNSDKNFPR	TVMVNLNIHN	RNTNTN..PK	RSSDYNRST	PWNLHRNED	62
IL-17B	NIEEMVAQLR	..NSSELAQR	KCEV....NL	QLWMSNKRSL	PWGYSINH	88
IL-17C	SLEAASHRGR	..HERPSATT	QPVLRPEEV	LEADTHQRSI	PWRYRVDTD	98
IL-17E	STVPVPPLP	..ARPNRHPE	S RASE....	.DGPLNSRAI	PWRYELDRD	65

2

3

IL-17F	PNRYPSEVVQ	AQ RNLG IN	A..QGKEDIS	MN VPI.QQE	TLVVRRKHQG	106
IL-17A	PERYPSVIWE	AK RHLG IN	A..DGNVDYH	MN VPI.QQE	ILVLRREPPH	109
IL-17B	PSRIPVDLPE	AR LCLG VN	PF.TMQEDRS	MV VPV.FSQ	VPVRRR...L	133
IL-17C	EDRYPQKLAF	AE LRG ID	AR.TGRETA	LN VRL.LQS	LLVLR...RP	144
IL-17E	LNRLPQDLYH	AR LPH VS	LQTGSHMDPR	GN ELLYHNQ	TVFYRRP...	112

4

\*

IL-17F	SV.....	....SFQLEK	VL..VTVGCT	CVTPIVHHVQ	...	133
IL-17A	PN.....	....SFRLEK	IL..VSVGCT	CVTPIVHHVA	...	136
IL-17B	CPPPPRTGP.	....CRQRA	VMETIAGCT	CIF.....	...	160
IL-17C	CSR DGSG LPT	PGAFAFHTEF	IH..VTVGCT	CV.LPRSVAA	ALE	184
IL-17E	CHGEKGTHKG	.....YCLER	RLYRVSLACV	CVRPRVMG..	...	145

FIG. 50

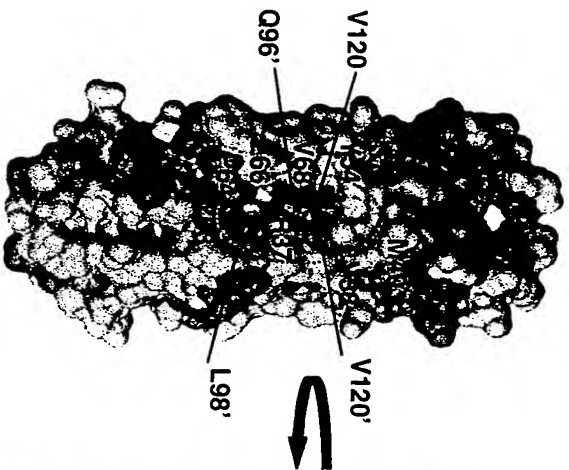


FIG. 51A

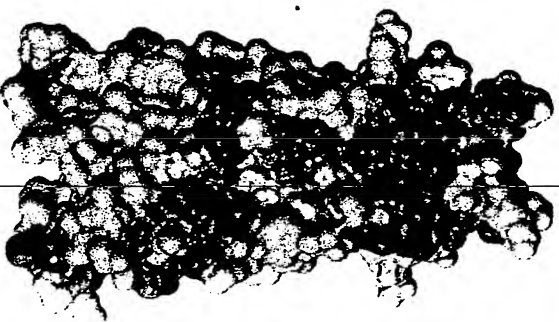


FIG. 51B



FIG. 51C

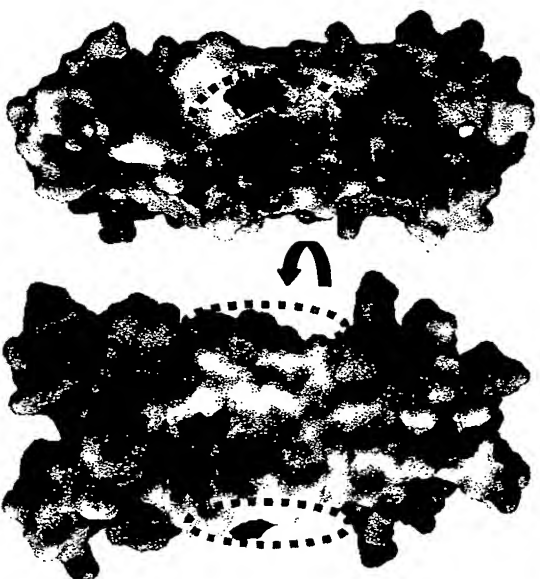


FIG. 52A

FIG. 52B



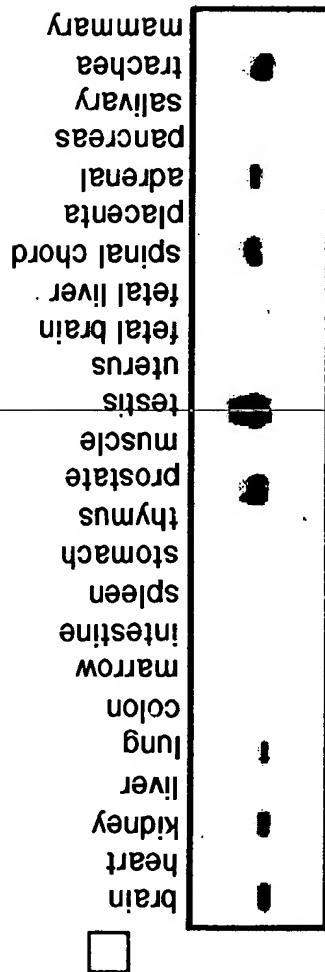
FIG. 52C

IL-17E is highly conserved between human and mouse

mIL-17E	1	-----	VAF	L	A	M	I	V	G	T	H	T	V	S	L	R	I	Q	E	G	C	S	H	L	P	S	C	C	P	S																					
hIL-17E	1	M	R	E	R	P	R	L	G	E	D	S	S	L	I	S	L	F	L	Q	V	V	A	F	L	A	M	V	M	G	T	H	T	-----	Y	S	H	W	P	S	C	C	P	S							
mIL-17E	35	K	E	Q	E	P	P	E	E	W	L	K	W	S	S	A	S	V	S	P	P	E	P	L	S	H	T	H	I	A	E	S	C	R	A	S	K	D	G	P	L	N	S	R	A	I	S	P	W	S	Y
hIL-17E	43	K	G	Q	D	T	S	E	E	L	L	R	W	S	T	V	P	V	P	P	L	E	P	A	R	P	N	R	H	P	E	S	C	R	A	S	E	D	G	P	L	N	S	R	A	I	S	P	W	R	Y
mIL-17E	85	E	L	D	R	D	L	N	R	V	P	Q	D	L	Y	H	A	R	C	L	C	P	H	C	V	S	L	Q	T	G	S	H	M	D	P	L	G	N	S	V	P	L	Y	H	N	Q	T	V	F	Y	R
hIL-17E	93	E	L	D	R	D	L	N	R	L	P	Q	D	L	Y	H	A	R	C	L	C	P	H	C	V	S	L	Q	T	G	S	H	M	D	P	R	G	N	S	E	L	L	Y	H	N	Q	T	V	F	Y	R
mIL-17E	135	R	P	C	H	G	E	E	G	T	H	R	R	Y	C	L	E	R	R	L	Y	R	V	S	L	A	C	V	C	V	R	P	R	V	M	A															
hIL-17E	143	R	P	C	H	G	E	K	G	T	H	K	G	Y	C	L	E	R	R	L	Y	R	V	S	L	A	C	V	C	V	R	P	R	V	M	G															

FIG. 53

# Tissue distribution of IL-17E



## IL-17E (PCR then probed with cDNA)

FIG. 54B

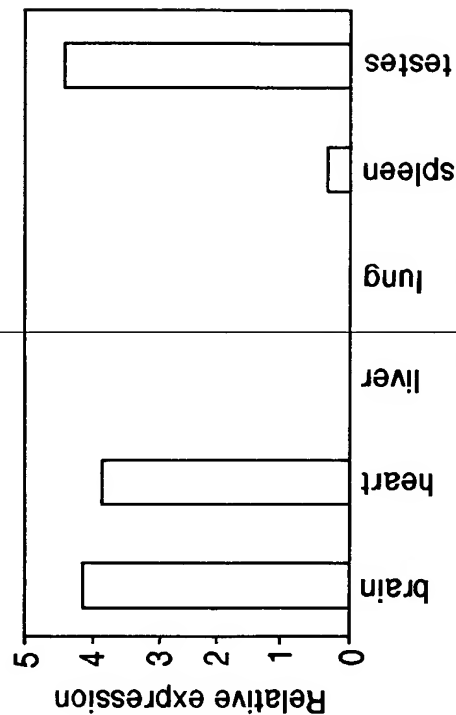


FIG. 54A

Mouse

mIL-17E transgenics are growth retarded

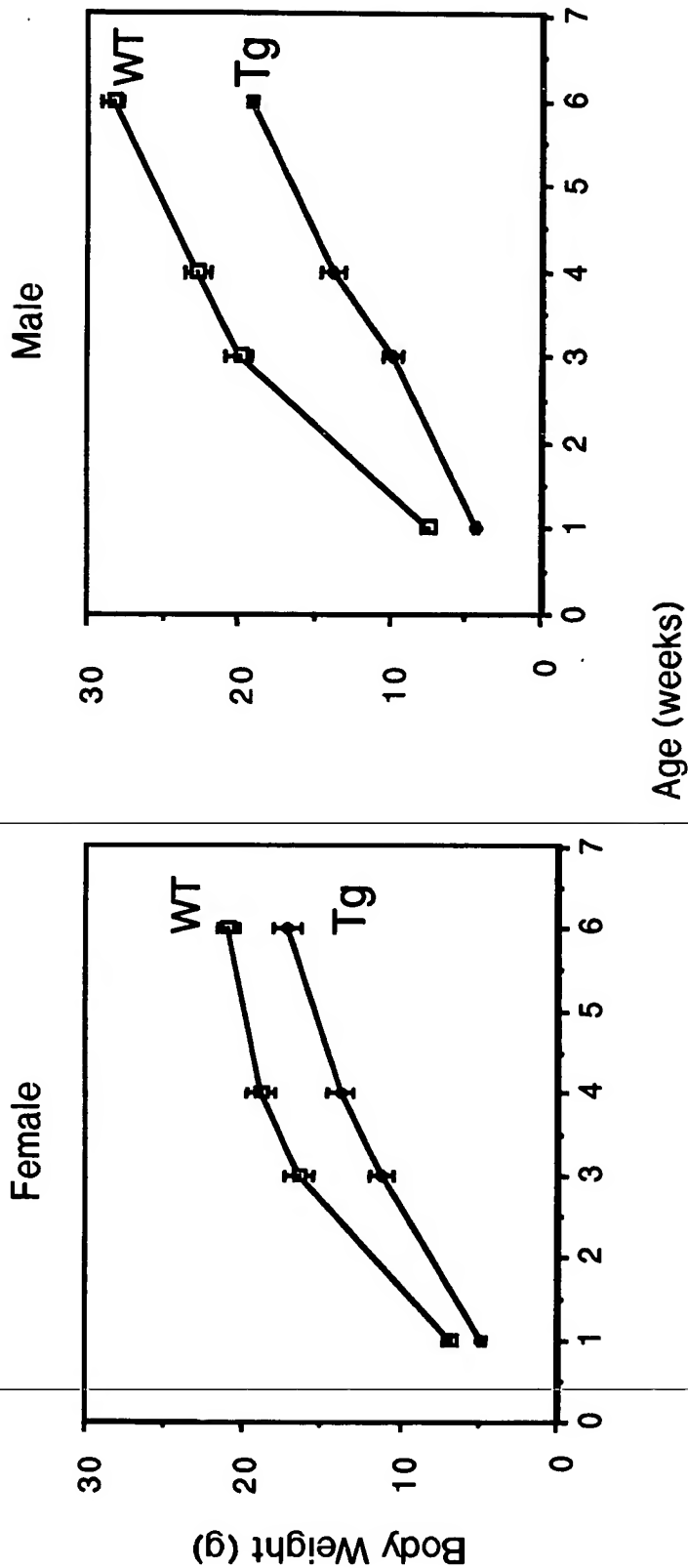
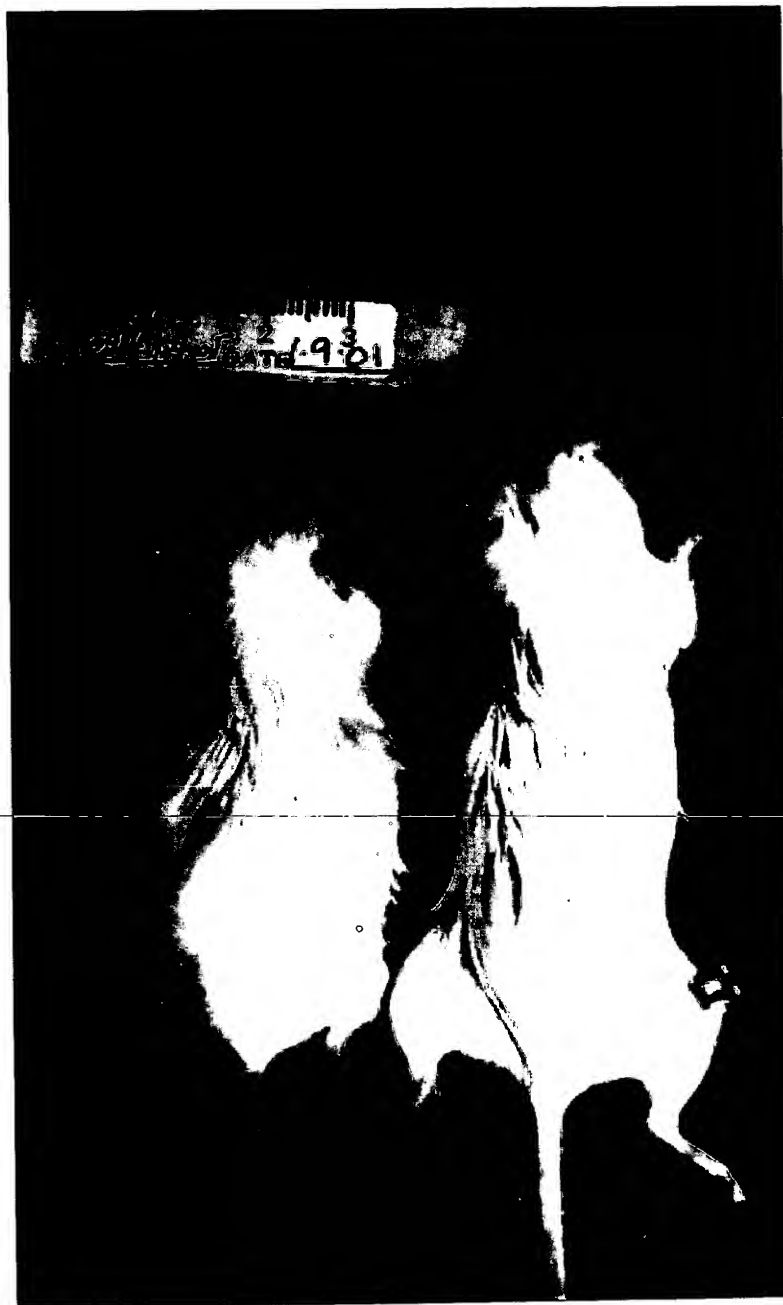


FIG. 55

IL-17E transgenics are jaundiced by 6 weeks of age



TG

WT

FIG. 56

mIL-17E transgenics have elevated total bilirubin and liver enzymes

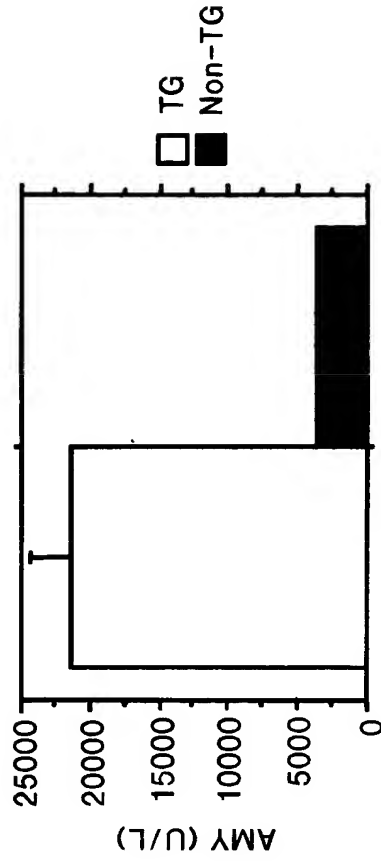
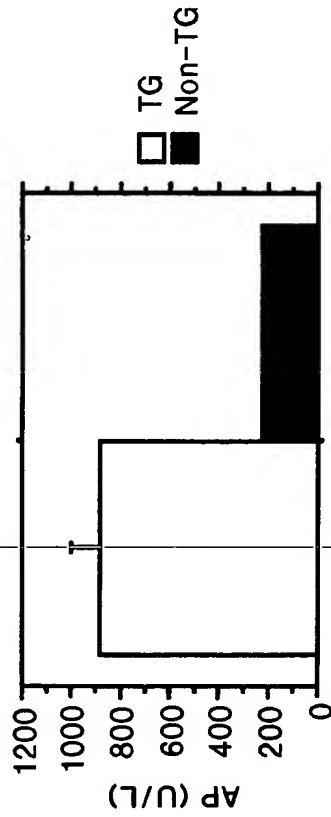
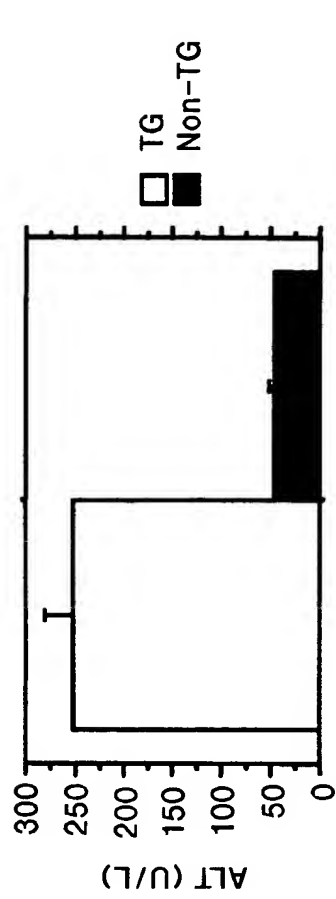
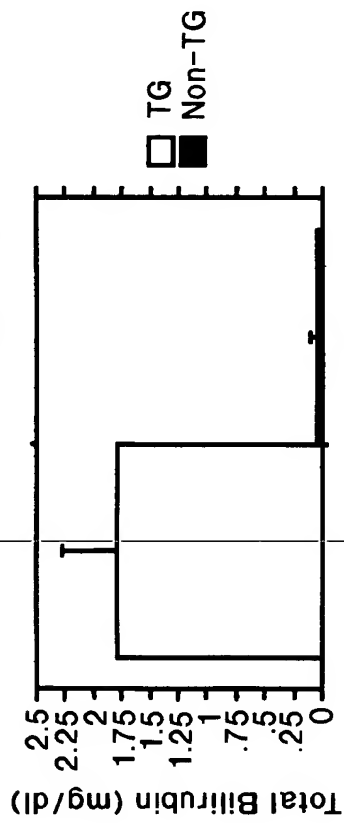


FIG. 57

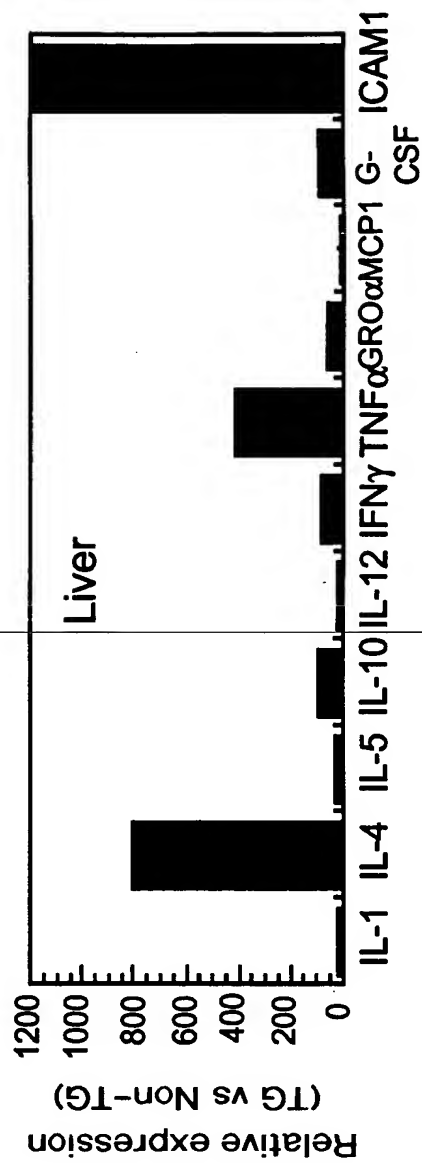


FIG. 58A

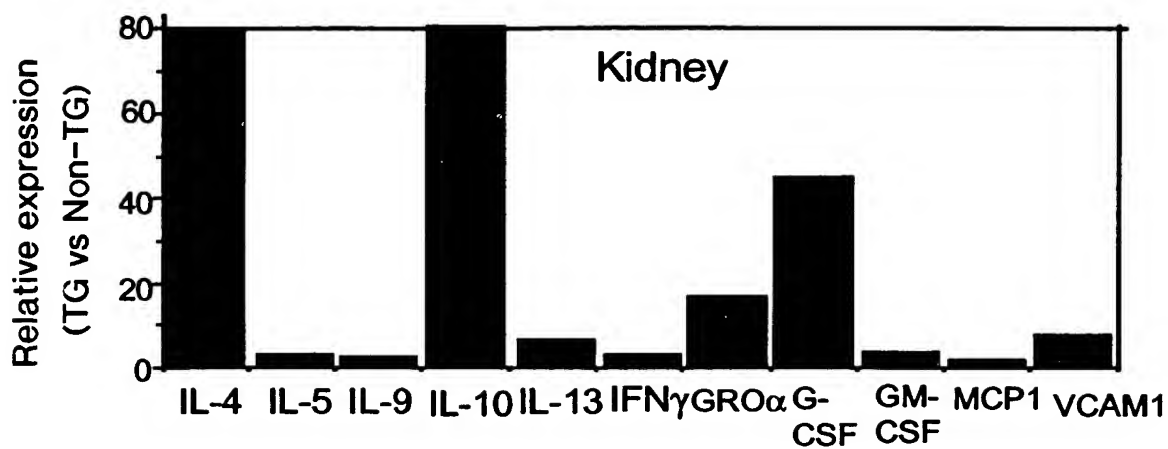


FIG. 58B

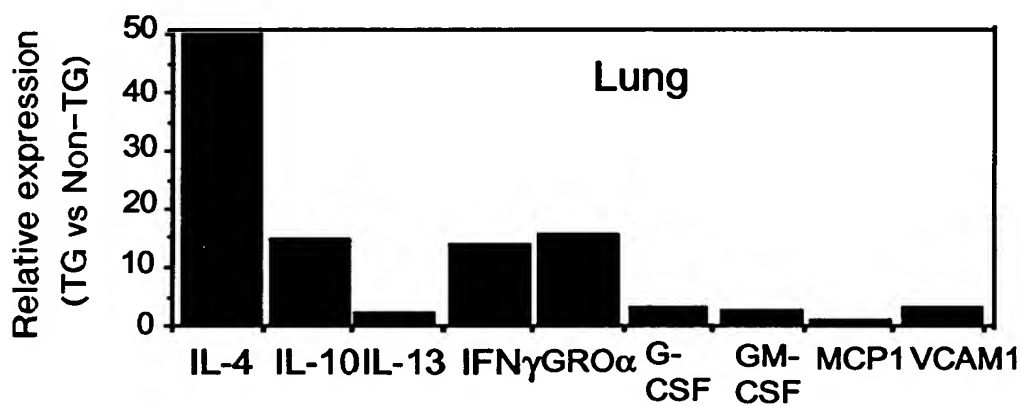
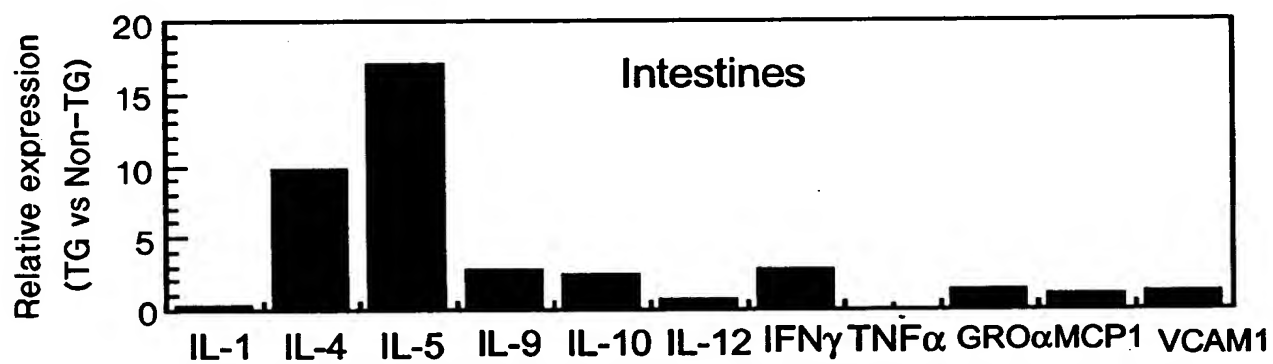
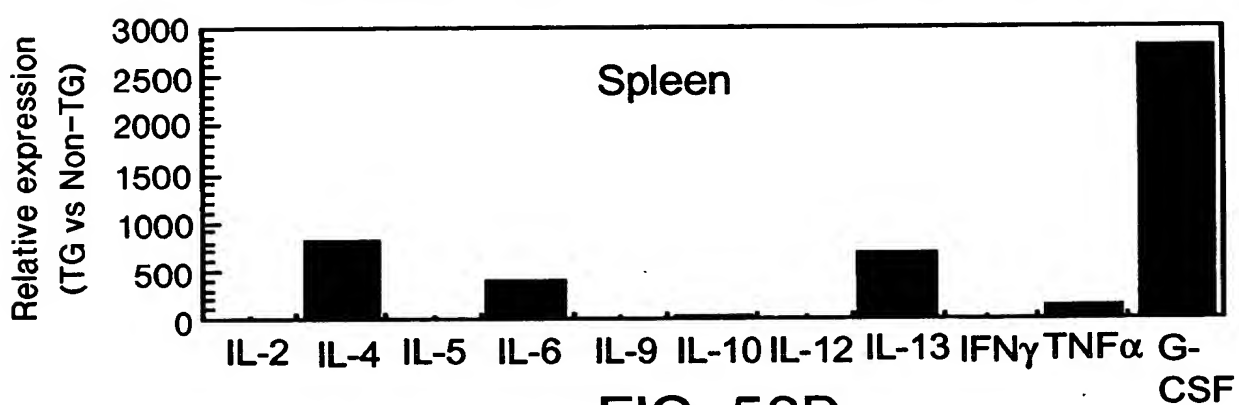


FIG. 58C

Gene profiling of IL-17E transgenics (Taqman)



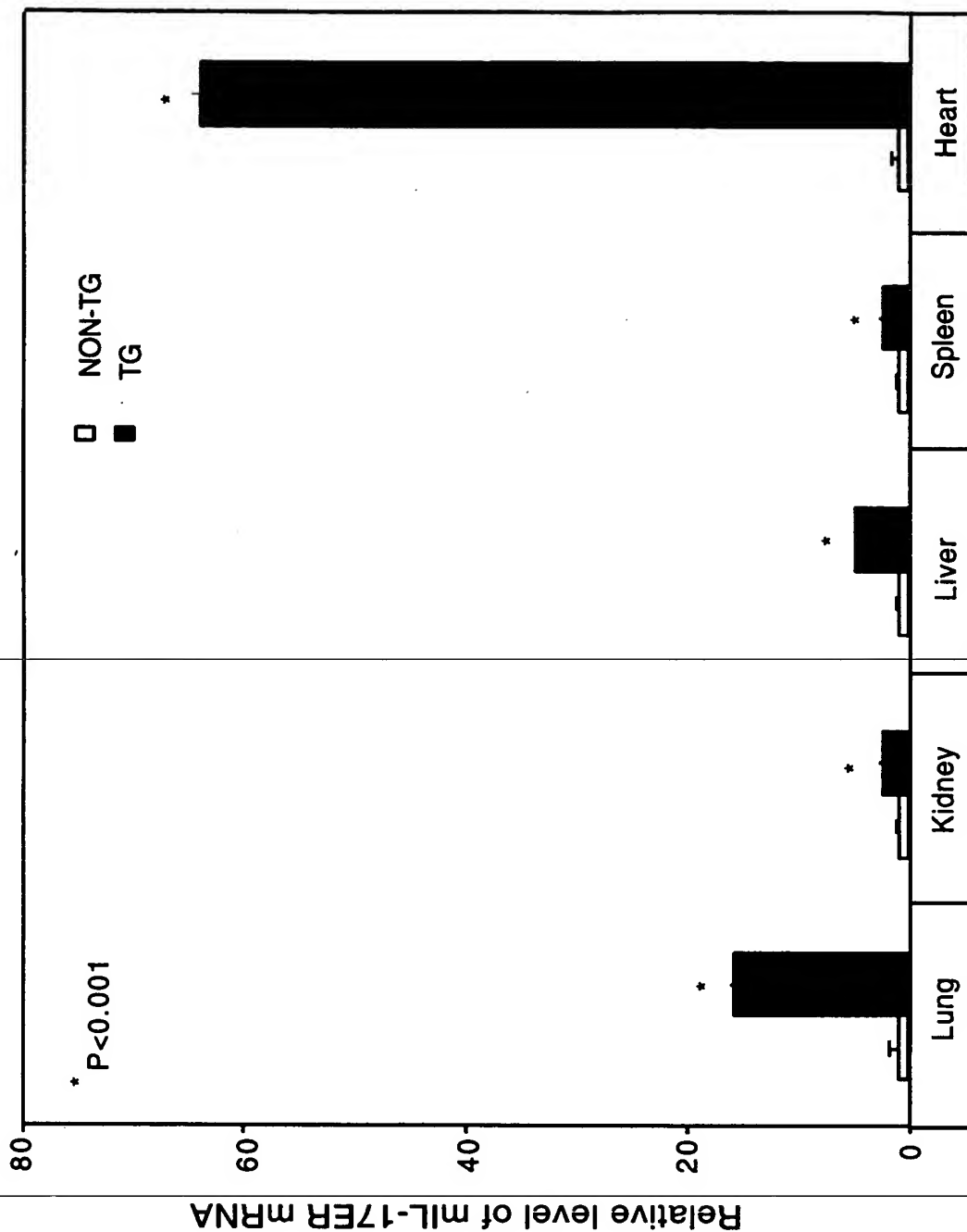


FIG. 59

Elevated serum IL-5, IL-13 and TNF  $\alpha$   
in mIL-17E transgenics

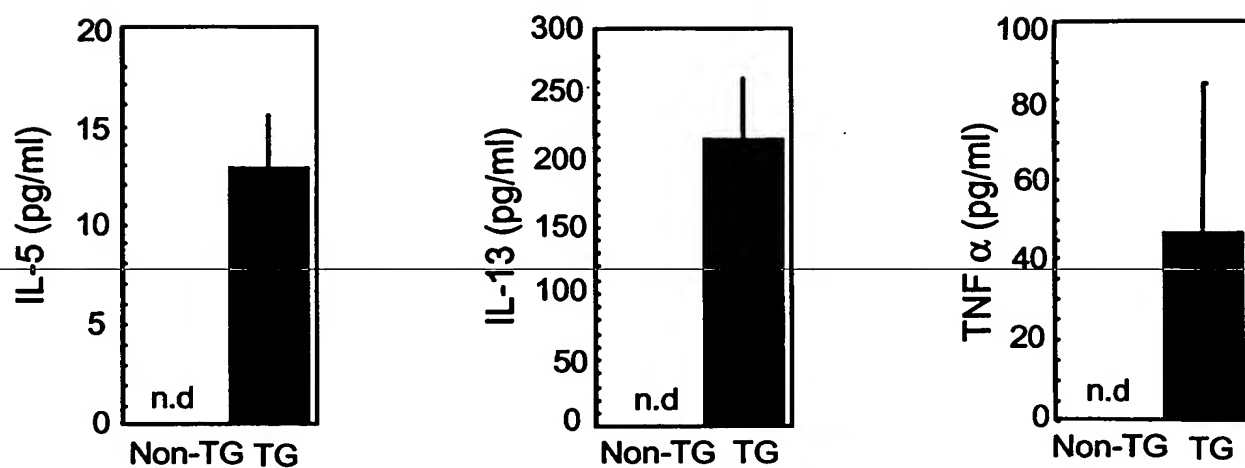


FIG. 60

Serum IgE and IgG1, but not IgG2a is elevated  
in mL-17E transgenics

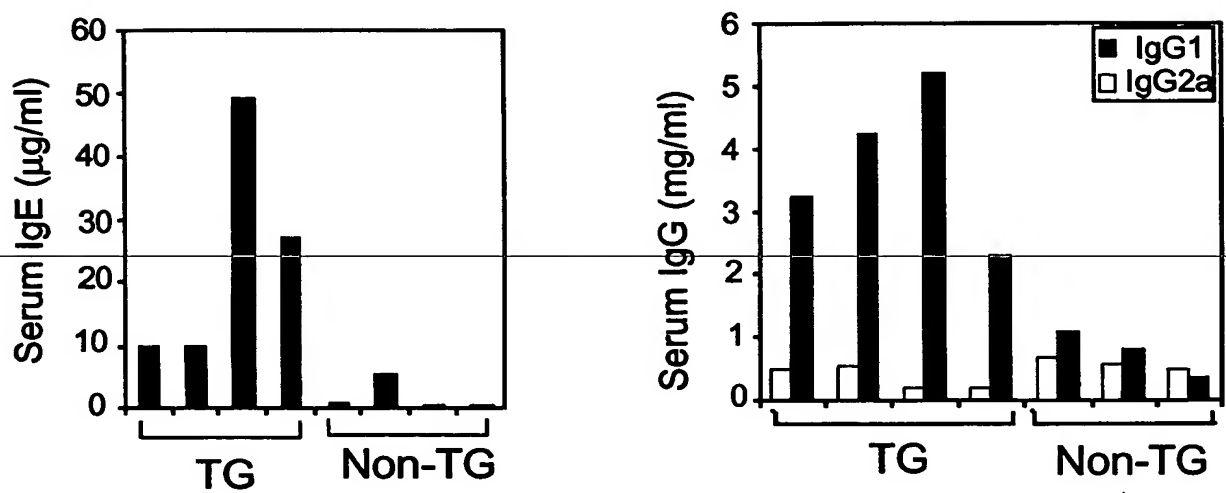


FIG. 61

Neutrophilia in mIL-17E transgenics  
(8 wks, PBMC by FACS)

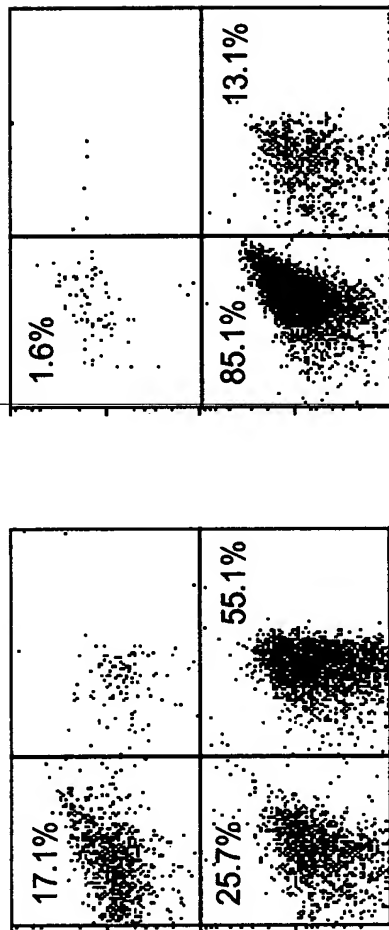


FIG. 62A

TG

FITC CD3

Non-TG

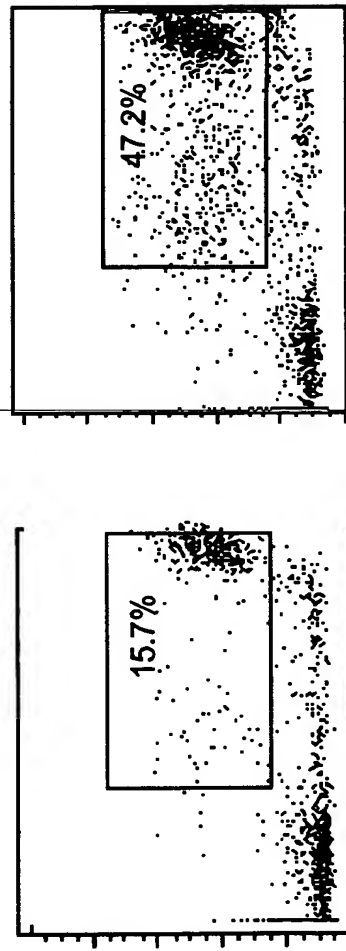


FIG. 62B

TG

PE GR-1

(neutrophils)

Non-TG

Neutrophilia and eosinophilia in mIL-17E  
transgenics (hematology)

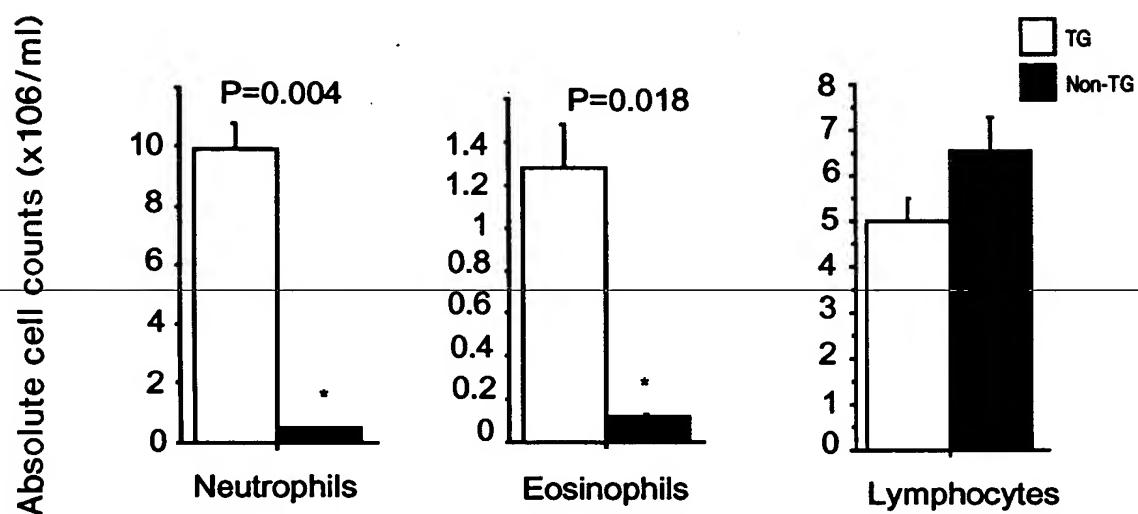


FIG. 63

G-CSF is elevated in  
mIL-17E transgenics

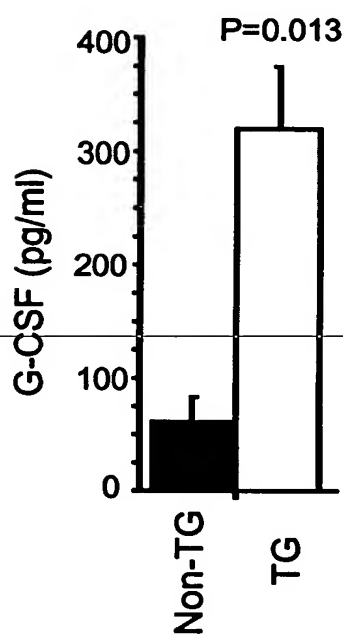
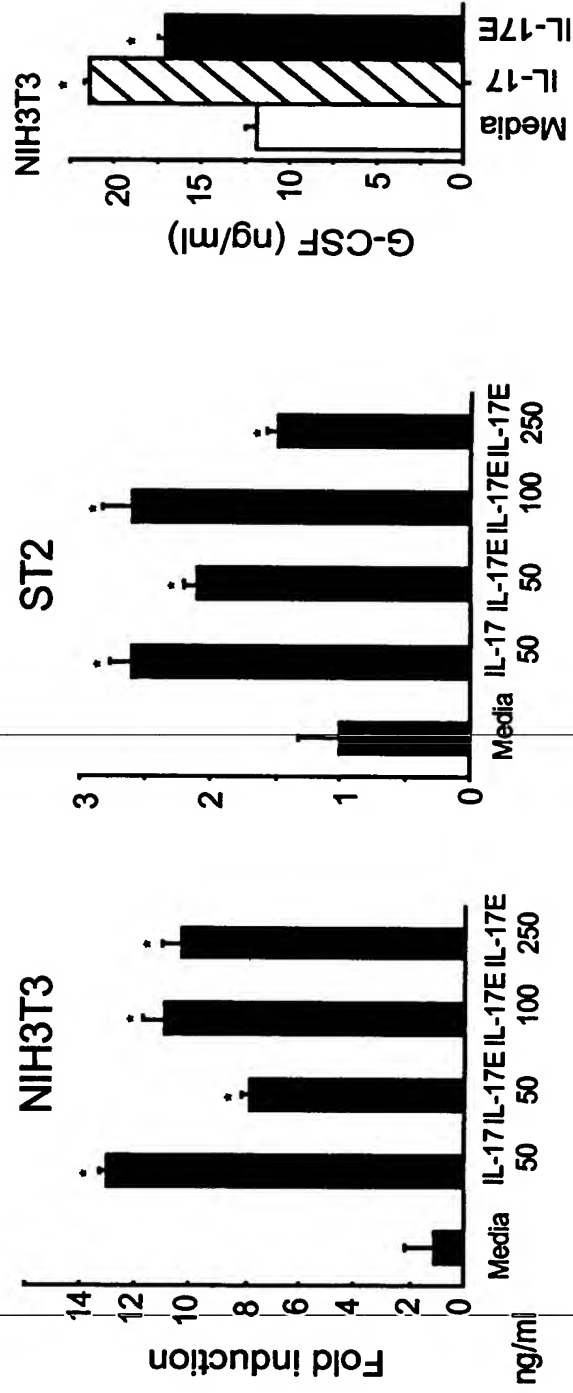


FIG. 64

# IL-17E induces production of G-CSF in vitro



\* $P < 0.05$

FIG. 65

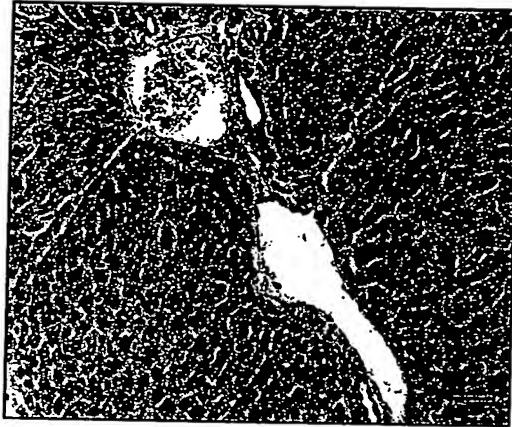


FIG. 66A



FIG. 66B

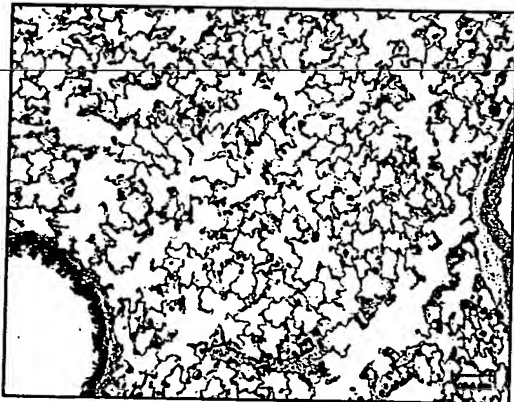


FIG. 66C

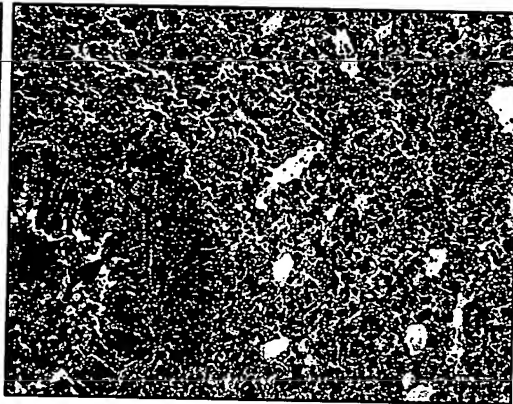


FIG. 66D